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OM nucleic - nucleic search, using sw model

Run on: February 19, 2004, 18:40:48 ; Search time 96 Seconds  
(without alignments)  
7272.169 Million cell updates/sec

Title: US-09-849-980B-2  
Perfect score: 1258  
Sequence: 1 GGCTCTGGACTGGGACACA.....AGCAAGGCTTGTCGACAAA 1258

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1258	100.0	1258	3	US-09-381-810A-2
2	179	14.2	536	4	US-09-621-976-17479
3	145.8	11.6	476	4	US-09-621-976-17480
4	124.2	9.9	912	4	US-09-252-991A-5479
5	124.2	9.9	2556	4	US-09-252-991A-5450
6	123.8	9.8	930	4	US-09-489-039A-3411
7	108.6	8.6	987	4	US-09-489-039A-2135
8	106.2	8.4	197	4	US-09-621-976-13266
9	105	8.3	960	4	US-09-489-039A-2828
10	89.8	7.1	636	4	US-09-252-991A-5464
11	78.4	6.2	849	4	US-09-543-681A-4103
12	78.4	6.2	2049	4	US-09-489-039A-3424
13	71.4	5.7	12145	3	US-08-968-563-19
14	71.4	5.7	12145	3	US-08-969-683A-19
15	71.4	5.7	12145	4	US-09-369-796-1
16	71.4	5.7	12145	4	US-09-307-973A-10
17	71.4	5.7	12145	4	US-09-641-652-1
18	60.6	4.8	1830121	4	US-09-557-884-1
19	60.6	4.8	1830121	4	US-09-643-990A-1
20	58.4	4.6	1408	1	US-08-447-554-3
21	58.4	4.6	1408	1	US-08-448-160-3
22	57.4	4.6	1081	4	US-09-372-422A-33
23	56.6	4.5	1116	4	US-09-372-422A-41
24	54	4.3	1375	4	US-09-372-422A-37
25	53.2	4.2	2520	4	US-08-961-527-226
26	50.4	4.0	1485	4	US-09-372-422A-39
27	49.8	4.0	939	4	US-09-252-991A-15282

c	28	49.8	4.0	1629	4	US-09-252-991A-15397	Sequence 15397, A
	29	49.8	4.0	2112	4	US-09-252-991A-15383	Sequence 15383, A
	30	49.8	4.0	12665	4	US-08-961-527-134	Sequence 134, Appl
	31	49.6	3.9	1069	4	US-09-372-422A-7	Sequence 7, Appli
	32	49.6	3.9	1333	4	US-09-372-422A-9	Sequence 9, Appli
	33	47	3.7	1206	4	US-09-372-422A-13	Sequence 13, Appl
	34	46	3.7	1158	4	US-09-372-422A-21	Sequence 21, Appl
	35	44.6	3.5	1217	4	US-09-372-422A-11	Sequence 11, Appl
	36	44.2	3.5	1153	4	US-09-372-448A-5	Sequence 5, Appli
c	37	44	3.5	7218	1	US-08-232-463-14	Sequence 14, Appl
	38	43.8	3.5	1304	4	US-09-372-422A-15	Sequence 15, Appl
	39	43.8	3.5	1384	4	US-09-372-422A-17	Sequence 17, Appl
	40	43.6	3.5	1193	4	US-09-372-422A-23	Sequence 23, Appl
	41	43	3.4	587	3	US-09-053-702-3	Sequence 3, Appli
	42	40.4	3.2	1204	4	US-09-372-422A-3	Sequence 3, Appli
	43	40.2	3.2	792	4	US-09-489-039A-4876	Sequence 4876, Ap
	44	40	3.2	720	4	US-09-134-001C-1328	Sequence 1328, Ap
	45	40	3.2	1242	4	US-09-372-448A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1  
US-09-381-810A-2  
; Sequence 2, Application US/09381810A  
; Patent No. 6252046  
; GENERAL INFORMATION:  
; APPLICANT: SANTEN PHARMACEUTICAL CO., LTD.  
; TITLE OF INVENTION: No. 6252046el Polypeptide Having Water Channel  
; TITLE OF INVENTION: Activity and DNA sequence  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SANTEN PHARMACEUTICAL CO., LTD.  
; STREET: 9 19 Shimoshinjo 3-chome Higashiyodogawa-Ku  
; CITY: Osaka  
; STATE: Osaka  
; COUNTRY: JAPAN  
; ZIP: 533-0021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB, storage  
; COMPUTER: IBM PS/2 or compatibles  
; OPERATING SYSTEM: WINDOWS 95/97  
; SOFTWARE: Microsoft Word 97  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/381,810A  
; FILING DATE: 19-OCT-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP09 094845  
; FILING DATE: 28-MAR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Burton A. Amernick  
; REGISTRATION NUMBER: 24852  
; REFERENCE/DOCKET NUMBER: 1581/00156  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)331-7111  
; TELEFAX: (202)293-6229  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1258 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; TISSUE TYPE: fat tissue  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: F173..1198  
; IDENTIFICATION METHOD: by experiment  
US-09-381-810A-2

priority doc.

Query Match 100.0%; Score 1258; DB 3; Length 1258;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTGGAAGTGGGACACAGGATAGCTGAGCCCGAGCTGGGGTGAAGCTGAGCCAG 60  
Db |||||||  
QY 1 GGCTTGGAAGTGGGACACAGGATAGCTGAGCCCGAGCTGGGGTGAAGCTGAGCCAG 60  
Db |||||||

QY 61 GGACAGTACAGGAGGAACAAGATCAAGATGCGGTGTAATCTGAGAGCCCCCAAGCGGAG 120  
Db |||||||

QY 61 GGACAGTACAGGAGGAACAAGATCAAGATGCGGTGTAATCTGAGAGCCCCCAAGCGGAG 120  
Db |||||||

QY 121 GCTGAGAAATCAGAGACATTTTCAGCAGACATCTACAAATCTGAAAGACAAACATGTTCA 180  
Db |||||||

QY 121 GCTGAGAAATCAGAGACATTTTCAGCAGACATCTACAAATCTGAAAGACAAACATGTTCA 180  
Db |||||||

QY 181 AGCATCCGGGCACAGCGGTCCACCGTGGTCCAAAATGGTCTCCTGGTCCGTGATAGC 240  
Db |||||||

QY 181 AGCATCCGGGCACAGCGGTCCACCGTGGTCCAAAATGGTCTCCTGGTCCGTGATAGC 240  
Db |||||||

QY 241 AAAGATCCAGGAAATACTGCAGAGGAAGATGGTGCAGAGATTCCTGGCCGAGTTTCATGAG 300  
Db |||||||

QY 241 AAAGATCCAGGAAATACTGCAGAGGAAGATGGTGCAGAGATTCCTGGCCGAGTTTCATGAG 300  
Db |||||||

QY 301 CACATATGTCATGATGGTATTCGGCTTGGTTCCTGGGCCCATATGGTTCTAAATFAAAAA 360  
Db |||||||

QY 301 CACATATGTCATGATGGTATTCGGCTTGGTTCCTGGGCCCATATGGTTCTAAATFAAAAA 360  
Db |||||||

QY 361 ATATGGGAGCTACCTTGGTGTCAACTTGGGTTTTGGCTTCGGAGTCACCATGGAGTGCA 420  
Db |||||||

QY 361 ATATGGGAGCTACCTTGGTGTCAACTTGGGTTTTGGCTTCGGAGTCACCATGGAGTGCA 420  
Db |||||||

QY 421 CGTGGCAGGCCGATCTCTGGAGCCACATGAACGAGCTGTGACCTTTGCTAACTGTGC 480  
Db |||||||

QY 421 CGTGGCAGGCCGATCTCTGGAGCCACATGAACGAGCTGTGACCTTTGCTAACTGTGC 480  
Db |||||||

QY 481 GCTGGCCGCGTCCCTGGAGGAAGTTTCCGGTCTATGTCTGGGSCAGTTCTCGGCTC 540  
Db |||||||

QY 481 GCTGGCCGCGTCCCTGGAGGAAGTTTCCGGTCTATGTCTGGGSCAGTTCTCGGCTC 540  
Db |||||||

QY 541 CTTCTGGCGGCTGCCACCATCTACAGTCTCTTCTACACGGCCATCTCCACTTTTCGGG 600  
Db |||||||

QY 541 CTTCTGGCGGCTGCCACCATCTACAGTCTCTTCTACACGGCCATCTCCACTTTTCGGG 600  
Db |||||||

QY 601 TGGACAGCTGATGTGACCGGTCCCGTGCCTACAGCTGGCATTTTGGCCACCTACCTTCC 660  
Db |||||||

QY 601 TGGACAGCTGATGTGACCGGTCCCGTGCCTACAGCTGGCATTTTGGCCACCTACCTTCC 660  
Db |||||||

QY 661 TGATCACATGACATTTGTGGCGGGCTTCTGAATGAGGCGTGGCTGACCGGATGCTCCA 720  
Db |||||||

QY 661 TGATCACATGACATTTGTGGCGGGCTTCTGAATGAGGCGTGGCTGACCGGATGCTCCA 720  
Db |||||||

QY 721 GCTGTGTCTCTTCGCCATCACGGACGAGAGAACACCCAGCACTGCCAGGAACAGAGGC 780  
Db |||||||

QY 721 GCTGTGTCTCTTCGCCATCACGGACGAGAGAACACCCAGCACTGCCAGGAACAGAGGC 780  
Db |||||||

QY 781 GCTGTGTATAGGCATCCTCGTGTCTATCATCGGGGTGTCCCTTGGCATGAACACAGGATA 840  
Db |||||||

QY 781 GCTGTGTATAGGCATCCTCGTGTCTATCATCGGGGTGTCCCTTGGCATGAACACAGGATA 840  
Db |||||||

QY 841 TGCCATCAACCCGCTCCCGGACCTGCCCCCGCATCTTCCACTTATTTGCTGGTGGG 900  
Db |||||||

QY 841 TGCCATCAACCCGCTCCCGGACCTGCCCCCGCATCTTCCACTTATTTGCTGGTGGG 900  
Db |||||||

QY 901 CAACAGGTCTTCAGCAATGGGAGAACTGGTGGGTGCCAGTGGTGCCACCTTCT 960  
Db |||||||

QY 901 CAACAGGTCTTCAGCAATGGGAGAACTGGTGGGTGCCAGTGGTGCCACCTTCT 960  
Db |||||||

QY 961 GGGTGCTATCTAGGTGGCATCATCTACCTGGTCTTCAATGGCTCCACCATCCCGAGGA 1020  
Db |||||||

QY 961 GGGTGCTATCTAGGTGGCATCATCTACCTGGTCTTCAATGGCTCCACCATCCCGAGGA 1020  
Db |||||||

QY 1021 GCCCTGAAATTTGGAGGATTCTGTGGCGTATGAAGACCACGGGATAACCGTATTGCCCAA 1080  
Db |||||||

QY 1021 GCCCTGAAATTTGGAGGATTCTGTGGCGTATGAAGACCACGGGATAACCGTATTGCCCAA 1080  
Db |||||||

QY 1081 GATGGGATCTCATGAACCCACGATCTCTCCCTCACCCTCTCTGTGAGCCCTGCGCAA 1140  
Db |||||||

QY 1081 GATGGGATCTCATGAACCCACGATCTCTCCCTCACCCTCTCTGTGAGCCCTGCGCAA 1140  
Db |||||||

QY 1141 CAGATCTTCAGTCCACCTGCCCCACCTTACATGAATCCATGCGCCCTAGAGCACTTCTA 1200  
Db |||||||

QY 1141 CAGATCTTCAGTCCACCTGCCCCACCTTACATGAATCCATGCGCCCTAGAGCACTTCTA 1200  
Db |||||||

QY 1201 AGCAGAGATTATTGTGATCCCATCCATTCGCCAATAAAGCAAGGCTTGTCCGACAAA 1258  
Db |||||||

QY 1201 AGCAGAGATTATTGTGATCCCATCCATTCGCCAATAAAGCAAGGCTTGTCCGACAAA 1258  
Db |||||||

RESULT 2  
US-09-621-976-17479  
; Sequence 17479, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 17479  
; LENGTH: 536  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-621-976-17479

Query Match 14.2%; Score 179; DB 4; Length 536;  
Best Local Similarity 97.0%; Pred. No. 1.9e-45;  
Matches 193; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1 GGCTCTGACTGGGGACACAGGGATAGCTGAGCCCGAGCTGGGGTGAAGCTGAGCCAG 60  
Db |||||||

QY 135 GGCTCTGACTGGGGACACAGGGATAGCTGAGCCCGAGCTGGGGTGAAGCTGAGCCAG 194  
Db |||||||

QY 61 GGACAGTACAGGAGGAACAAGATCAAGATGCGGTGTAATCTGAGAGCCCGGAG 120  
Db |||||||

QY 195 GGACAGTACAGGAGGAACAAGATCAAGATGCGCTTAACTGAGAGCCCGGAG 254  
Db |||||||

QY 121 GCTGAGAAATCAGA-GACATTTTCAGCAGACATCTACAAATCTGAAAGACAAACATGGTTC 179  
Db |||||||

QY 255 GCTGAGAAATCAGAAGACATTTTCAGCAGACATCTACAAATCTGAAAGACAAACATGGTTC 314  
Db |||||||

QY 180 AAGCATCCGGGCACAGGCG 198  
Db |||||||

QY 315 AAGCATCTGGGCACAGGCG 333  
Db |||||||

RESULT 3  
US-09-621-976-17480  
; Sequence 17480, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 17480

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; LENGTH: 476
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-17480

Query Match      11.6%; Score 145.8; DB 4; Length 476;
Best Local Similarity 95.5%; Pred. No. 3.4e-35;
Matches 150; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGCTCTGGACTGGGGACACAGGATAGCTGAGCCCCAGCTGGGGGTGGAAGCTGAGCCAG 60
Db 132 GGCTCTGGACTGGGGACACAGGATAGCTGAGCCCCAGCTGGGGGTGGAAGCTGAGCCAG 191
QY 61 GGACAGTCACGGAGGAACAAGATCAAGATGCGCTGTAAGTGAAGAGCCCCCAAGGGGAG 120
Db 192 GGACAGTCACGGAGGAACAAGATCAAGATGCGCTGTAAGTGAAGAGCCCCCAAGGGGAG 251
QY 121 GCTGAGAATCAGAGACATTTTCAGCAGACATCTACAAA 157
Db 252 GCTGAGAATCAGAGACATTTTCAGCAGAGATCTCTGGACA 288

RESULT 4
US-09-252-991A-5479
; Sequence 5479, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5479
; LENGTH: 912
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5479

Query Match      9.9%; Score 124.2; DB 4; Length 912;
Best Local Similarity 50.1%; Pred. No. 2.5e-28;
Matches 374; Conservative 0; Mismatches 358; Indels 15; Gaps 2;

QY 270 TGGTGGAGAGTTCTCTGGCCGAGTTTCATGAGCACATATGTATGATGGTATTCGGCCCTTG 329
Db 101 TGTTCGGCCCAATGCCTGGCCGAGTTCTCTCGGACCGCCCTCTCATCTTCTTCGGCACCG 160
QY 330 GTTCCGTTGGCCCATATGTTTCTAAATAAAAATATGGGAGCTACCTTGGTGTCAACTTGG 389
Db 161 GTTTCGTTGGCCCTGAAGGTCGGCCGCGCCAGCTTCGGCCCTGTGGGAATCAGCATCA 220
QY 390 GTTTTGGCTTCGGAGTCACCATGGGAGTGCACGTGGCAGGCGCATCTCTGGAGCCCCACA 449
Db 221 TCTGGGGGTTCGGCGTGAGCATGGCGATCTACCTCAGCGCGCGGTCTCCGGCGCCACC 280
QY 450 TGAACGCAGCTGTGACCTTTGCTAACTGTGCGCTGGGCGCGGTGCCCTGGAGGAAGTTTC 509
Db 281 TGAACCGCGGTGAGCATCGCGCTGTGGCTGTTCGCGGCTTCGAGGGGCGCAAGCTGC 340
QY 510 CGGTCTATGTCTGGGGCAGTTCTCTGGGCTCTCTCTGGCGGCTGCCACCATCTACAGTC 569
Db 341 CGTTCTACATCACCGCCAGGTGGCGGCTGCGTTCTGCGCGCAGCGCTGTGTCTACACCC 400
QY 570 TCTTCTACAGGCCATTCTCCACTTTTCGGGTGGACAGCTGATGGTGACCCG----- 621
Db 401 TCTACAGCAGCCTGTTTCATCAGATTTCGAACAGGCGCAGAAATCGTCCGCGCAGCCAGG 460
QY 622 -TCCCGTCGCTACAGCTGGCATTTTGGCCACCTACCTTCTCTGATCACAATGACATTGTGGC 680
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Db 461 ACAGCCTGGCCCTGGCCTCGGTGTTCTCCACCTATCCGACCCCGCGCTGTGGTGGCC 520
QY 681 GGGGCTTCTGTAATGAGGCGTGGCTGACCGGATGCTCCAGCTGTGTCTCTTCGCCATCA 740
Db 521 AGGCGTTCTCTGTCGAAGTGGTGATCACGGCCATCCTCATGGCGGTGATCATGGCCCTTA 580
QY 741 CGGACGAGAGAAACAACCCAGCACTGCCAGAAACAGAGCGCTGGTGATAGGCATCTCTCG 800
Db 581 CCGACGAGCGCAACCGCCTGCCGCGGTCCGTTGGCGCGCTGCTGATCGGCTGCTGA 640
QY 801 TGGTCATCATCGGGGTGTCCTTTGGCATGAACAACAGGATATGCCATCAACCCGTCGCCGG 860
Db 641 TCGCGTGATCGGTAGCGCCATGGGCCCTGACCGGTTTCGGCATGAACCCGGCGCG 700
QY 861 ACCTGCCCCCGCATCTTCACCTTCACTTCTGCTGGTTGGGCAACAGGTCTTCA----- 914
Db 701 ACTTCGGCCCCAAGCTGATGACCTACCTGGCGGCTGGGGGCCCATCGCCTTCACCGCG 760
QY 915 GCAATGGGAGAACTGGTGGTGGTGCCAGTGGTGACCACTTCTGGGTGCTCTATCTAG 974
Db 761 GCGCGGAGATTCCCTATTCTTCTGGTGCGCATCTTCGCCCGCATCTTCGGTGCCTGCTCG 820
QY 975 GTGGCATCATCTACCTGGTCTTCAATTG 1001
Db 821 GCGCGCGCGCTATCGTGTACTGATCG 847

RESULT 5
US-09-252-991A-5450/c
; Sequence 5450, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5450
; LENGTH: 2556
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5450

Query Match      9.9%; Score 124.2; DB 4; Length 2556;
Best Local Similarity 50.1%; Pred. No. 4.6e-28;
Matches 374; Conservative 0; Mismatches 358; Indels 15; Gaps 2;

QY 270 TGGTGGAGAGTTCTCTGGCCGAGTTTCATGAGCACATATGTATGATGGTATTCGGCCCTTG 329
Db 2483 TGTTCGGCCAATGCCTGGCCGAGTTCTCTCGGACCGCCCTCTCATCTTCTTCGGCACCG 2424
QY 330 GTTCCGTTGGCCCATATGTTTCTAAATAAAAATATGGGAGCTACCTTGGTGTCAACTTGG 389
Db 2423 GTTTCGTTGGCGCCCTGAAGGTCGCGCGCGCCAGCTTCGGCCTGTGGGAATCAGCATCA 2364
QY 390 GTTTTGGCTTCGGAGTCAACATGGGAGTGCACGTGGCAGGCGCATCTCTGGAGCCCCACA 449
Db 2363 TCTGGGGGTTCGGCGTGAGCATGGCGATCTACCTCAGCGCGCGGTCTCCGGCGCCACC 2304
QY 450 TGAACGCAGCTGTGACCTTTGCTAACTGTGCGCTGGGCGCGTGGCGCGCTGCCCTGGAGGAAGTTTC 509
Db 2303 TGAACCGCGCGGTGAGCATCGCGCTGTGGCTGTTCGCCGCTTCGAGGGGCGCAAGCTGC 2244
QY 510 CGGTCTATGTCTGGGGCAGTTCTCTGGGCTCTCTCTGGGCTCTCTCTGGCGGCTGCCACCATCTACAGTC 569
Db 2243 CGTTCTACATCACCGCCAGGTGGCGGCTGCGTTCTGCGCGCAGCGCTGGTCTACACCC 2184
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QY	570	TCTTCTACAGGCGCATCTTCCACTTTTTCGGGTGGACAGCTGATGGTGACCGG-----	621
Db	2183	TCTACAGCAGCGCTGTTTCATCGAGTTCGAACAGGCGCAGAACATCGTCCGGCGGAGCCAGG	2124
QY	622	-TCCCGTCGTACAGCTGGCATTTTGTGCCACTACCTTCCTGATCACATGACATTGTGGC	680
Db	2123	ACAGCCTGGCCCTGGCCCTCGGTGTTCTCCACTATCCGCACCGGGCGCTCTCGGTCGGCC	2064
QY	681	GGGGCTTCCTGAATGAGGCGTGGCTGACCGGGATGCTCCAGCTGTGTCTCTTCGCCATCA	740
Db	2063	AGGCGTTCCTCGTCGAAGTGTGATCACGGCCATCCTCATGGCGGTGATCATGGCCCTTA	2004
QY	741	CGGACCAGGAGAACAAACCCAGCACCTGCCAGGAACAGAGGCGCTGGTGATAGGCATCCTCG	800
Db	2003	CCGACGACGGCAACGGCCCTGCCGCGCGGTCCGTTGGCGCCGCTGCTGATCGGCGTGTGA	1944
QY	801	TGGTCATCATCGGGGTGTCCCTTGGCATGAACACAGGATATGCCATCAACCGTCCCGGG	860
Db	1943	TCGCCGTGATCGGTAGCGCATGGGCCCGCTGACCGGTTTCGCGATGAACCGGGCGCGG	1884
QY	861	ACCTGCCCCCGGCATCTTCACCTTCATTGCTGGTTGGGGCAACAGGTCCTCA-----	914
Db	1883	ACTTCGGCCCCAAGCTGATGACCTACCTTGCGCGGCTGGGGGCCCATCGCCCTTCACCGGG	1824
QY	915	GCAATGGGGAGAACTGGTGTGGGTGCCAGTGGTGGCACCACTTCTGGGTGCCATCTAG	974
Db	1823	GCCGCGAGATTCCCTATTTCTCGGTGCCGATCTTCGCCCCCGATCCTCGGTGCCCTGCTCG	1764
QY	975	GTGGCATCATCTACCTGGTCTTCATTG	1001
Db	1763	GCGCCGGCGGTATCGTACTGATCG	1737

## RESULT 6

US-09-489-039A-3411  
; Sequence 3411, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 3411  
; LENGTH: 930  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-3411

Query Match	9.8%	Score 123.8;	DB 4;	Length 930;
Best Local Similarity	49.8%;	Pred. No. 3.4e-28;		
Matches 379;	Conservative	0;	Mismatches 367;	Indels 15;
				Gaps 2;

Qy	279	AGTTCCTGGCCGAGTTTCATGAGCACATATGTCATGATGGTATTCCGCCCTTGCTTCCGTGG	338
Db	107	AGTGCAATCGCAGAGTTCTCTCGGTACCGGGTTGTTGATCTTTTTCGGCGTTTGGGTGCGTGG	166
	339	CCCATATGGTTCATAATAAAAAATATGGGAGCTACCTTGGTGTCAACTTGGGTTTTTGGCT	398
Db	167	CTGCGCTCAAGGTCGGGGAGCCAGCTTCGGACAATGGGAATCAGCATCATCTGGGGTC	226
Qy	399	TCGGAGTCACCATGGGAGTGCACGTGGCAGGCCGCATCTCTGGAGCCCCACATGAACGCAG	458
Db	227	TGGGCGTCGCCATGGCGATCTACCTGACCGCGGGGTCTCCGGTGGCACCTTAACCCAG	286
Qy	459	CTGTGACCTTTGCTAACTGTGCGCTGGGCCGGCTGCCCTGGAGGAAGTTTCCGGTCTATG	518
Db	287	CGGTGACTATCGCGCTGTGGCTGTTTCGCTGTTCGAAGGCCGCAAGTGGTTCCTTTTA	346

QY	519	TGCTGGGGCAGTTCTCTGGGCTCCTTCTGGCGGCTGCCACCATCTACAGTCTCTTTACACA	578
DB	347	TTATTTTCGCAATTCTGGCGGCTTTTGGCTGCGGCATTAGTTTACGGGCTTTACTACA	406
QY	579	CGGCCATTCTCCACTTTTTCGGGTGGACAGCTGATGGTGAACCGGTCCCG-----TCG	629
DB	407	ATCTTTTCTCGAATTATGAACACCCACCATATGATTTCGGCGAGCGTGGAAAGCCTCG	466
QY	630	CTACAGCTGGCAATTTTGGCCACTACTTCTTGATCACAATGTGGCGGGGCTTCC	689
DB	467	ATCTGGCCGGCAATTTCTCCACTTACCCGAACCGGCACATCAATTTGTGCAAGGCCCTCG	526
QY	690	TGAATGAGCGTGGCTGACCCGGGATGCTCCAGTGTGTCTCTTCGCCATCACGGACCAAG	749
DB	527	CGGTAGAGATGGTGATTACCGCTATCCTGTATGGGCGTCACTCTGGGCGTGACCGACGATG	586
QY	750	AGAACAAACCCAGCACTGCCAGGAACAGAGGCGTGGTGATAGGCATCCTCGTGGTCAACA	809
DB	587	GCAACGGCATACCGCGCGCCCGCTGGCCCTCTGCTGATTGGCCTGCTGATTGCGGTGA	646
QY	810	TCGGGGTGTCCCTTGGCATGAACACAGGATATGCCATCAACCCCGTCCCGGACCTGCCCC	869
DB	647	TGGCGCCTCCATGGGACCGCTGACCGGCTTCGCCATGAACCCGCGCGTGACATCGGCC	706
QY	870	CCCGCATCTTCACTTTCATTGTCTGGTTGGGGCAACAGGTCTTTCA-----GCAATGGGG	923
DB	707	CGAAAGCCTTCGCTTGGCTGGCGGGGTGGGTGACGTCGCCCTTCACTGGCGGCAAGATA	766
QY	924	AGAACTGGTGGGTGCCAGTGGTGGCACCACTTCTGGGTGCCTATCTAGGTGGCATCA	983
DB	767	TTCTTTATTTCTGGTGCCGCTGTGCGCACCGGTGGTTCGGCGCGCGCTGGGCGCATCA	826
QY	984	TCTPACCTGGTCTTCAATTGGCTCCACCATTCCCAACGGGAGCCC	1024
DB	827	GCTATCGTAAGCTGATTGGCCGTCACCTGCTTGGGACACC	867

## RESULT 7

US-09-489-039A-2135  
; Sequence 2135, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 2135  
; LENGTH: 987  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-2135

Query Match	8.6%	Score 108.6;	DB 4;	Length 987;
Best Local Similarity	48.6%;	Pred. No. 1.8e-23;		
Matches 368;	Conservative	0;	Mismatches 374;	Indels 15; Gaps 2;

QY	279	AGTTCTCTGGCCGAGTTCATGAGCACATATGTCATGATGGTATTCGGGCTTGGTTCCGTGG	338
Db	212	AGTGGCTGGCCGAGTTCTTGGCACCGGATTGCTCATTTTCTTCGGCGGGCTGCGTCG	271
QY	339	CCCATATGGTTCTAAATAAAAAATATGGGAGCTACCTTGGTGTCAACTTGGGTTTTCGCT	398
Db	272	CTGGCGCTCGGGTCGCCGGGCCAGCTTTGGTCAGTGGGAGATCAGTATTATCTGGGGCC	331
QY	399	TCGGAGTCAACATGGGAGTGCACTGGCAGGCCCGCATCTCTGGAGCCACATGAACGCAG	458
Db	332	TGGCGTTCGCGATGGCCACTACTGACGGCCGGTGTCTCCGGCGGCACCTTAATCCGG	391





QY 990 TGGTCTTCAATGGCTCCACCATCCACGGAGGCC 1024  
| | | | | | | | | | | | | | | | | |  
Db 899 GTTTCTTATCGCCAATAATCTGCCCTGTCTATACC 933  
| | | | | | | | | | | | | | | | | |

RESULT 10

US-09-252-991A-5464  
; Sequence 5464, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 5464  
; LENGTH: 636  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-5464.

Query Match 7.1%; Score 89.8; DB 4; Length 636;  
Best Local Similarity 49.2%; Pred. No. 9.6e-18;  
Matches 272; Conservative 0; Mismatches 272; Indels 9; Gaps 1;

QY 270 TGGTGGGAGATTCTTGGCGGAGTTTCATGAGCAGCATATGTCAATGATGTTTGGGCTTTG 329  
| | | | | | | | | | | | | | | | | |  
Db 81 TGTTGGGCAATGCTTGGCGGAGTTCTCGGACCGCCCTCTCTCATCTTCTTGGGACCG 140  
| | | | | | | | | | | | | | | | | |  
QY 330 GTTTCGGTGGCCCATATGTTCTTAATAAAAAATATGGGAGCTACCTTGGTGTCAACTTGG 389  
| | | | | | | | | | | | | | | | | |  
Db 141 GTTGGTGGCGGCTGAAGGTTCGGCGGCGGAGCTTGGGCTTGGGAAATCAGCATCA 200  
| | | | | | | | | | | | | | | | | |  
QY 390 GTTTTGGCTTCGGAGTCAACCATGGAGTGCAAGTGGCAGGCGGATCTCTGGAGCCCA 449  
| | | | | | | | | | | | | | | | | |  
Db 201 TCTGGGGGTTCGGGTGAGCATCGGCTGTGGCTTTCGCCCGGCTTCGGGCGGCCACC 260  
| | | | | | | | | | | | | | | | | |  
QY 450 TGAACGCAGCTGTGACCTTTGCTAACTGTCGCTGGGCGGCGGCTGGAGGAAATTTTC 509  
| | | | | | | | | | | | | | | | | |  
Db 261 TGAACCGCGGCTGAGCATCGGCTGTGGCTTTCGCCCGGCTTCGAGGGGCGCAAGCTGC 320  
| | | | | | | | | | | | | | | | | |  
QY 510 CGGTCTATGTGCTGGGCGAGTTCTTGGGCTCTTCTGGGCGGCTGCCACCATCTACAGTC 569  
| | | | | | | | | | | | | | | | | |  
Db 321 CGTTCTACATCACCGCCAGGTGGCGGCTGCTTCTGCGCGGCGGCTGCTTACACCC 380  
| | | | | | | | | | | | | | | | | |  
QY 570 TCTTCTACACGGCCATTCTCCACTTTTTCGGTGGAAGCTGATGGTGACCGG----- 621  
| | | | | | | | | | | | | | | | | |  
Db 381 TCTACAGCAGCTGTTCATCGAGTTTCGAAACAGGCGCAGAACATCGTTCGGCGGAGCCAGG 440  
| | | | | | | | | | | | | | | | | |  
QY 622 -TCCCGTTCGCTACAGCTGGCATTTTTCGACCTTCTGATCAGATGACATGATGTCGC 680  
| | | | | | | | | | | | | | | | | |  
Db 441 ACAGCCTTGGCCCTGGGCTCGGTGTTCTCCACCTATCCGACCCCGGCGCTGTGCGTGGCC 500  
| | | | | | | | | | | | | | | | | |  
QY 681 GGGGCTTCTGAATGAGGCGGTGGTGACCGGATGCTCCAGCTGTGCTCTTTCGCGCATCA 740  
| | | | | | | | | | | | | | | | | |  
Db 501 AGGCGTTCCTCGTCGAAGTGGTGATCAGGCGCATCTCTCATGGCGGTGATCATGGCCCTTA 560  
| | | | | | | | | | | | | | | | | |  
QY 741 CGGACAGGAGAAACACCCAGCACTGCGCAGGAAACAGAGGCGCTGGTGATAGGCACTCTCG 800  
| | | | | | | | | | | | | | | | | |  
Db 561 CCGACGACGGCAACGGCTTCCCGCGCGGTCCGTTGGCGCGGCTGCTGATCGGCTGCTGA 620  
| | | | | | | | | | | | | | | | | |  
QY 801 TGGTCATCATCGG 813  
| | | | | | | | | | | | | | | | | |  
Db 621 TCGCGGTGATCGG 633  
| | | | | | | | | | | | | | | | | |

RESULT 11

US-09-543-681A-4103  
; Sequence 4103, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; FILE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 4103  
; LENGTH: 849  
; TYPE: DNA  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-4103

Query Match 6.2%; Score 78.4; DB 4; Length 849;  
Best Local Similarity 45.9%; Pred. No. 3.9e-14;  
Matches 357; Conservative 0; Mismatches 406; Indels 15; Gaps 2;

QY 273 TCGGAGAGTTCCTGGCGGAGTTTCATGAGCAGCATATGTCAATGATGTTTGGGCTTTGGTT 332  
| | | | | | | | | | | | | | | | | |  
Db 59 TGGGTCAATGCATTTCCGAGTTTATCGGTACTGCTAGTCTTCTTTGGTCTTGGTT 118  
| | | | | | | | | | | | | | | | | |  
QY 333 CCGTGGGCCCATATGTTCTTAATAAAAAATATGGGAGCTACCTTGGTGTCAACTTGGGTT 392  
| | | | | | | | | | | | | | | | | |  
Db 119 GTGTTGAGCAGCAGCATATCGCAGGCGCTCAACTCGGTCTTTGGGAGATAAGTATTATCT 178  
| | | | | | | | | | | | | | | | | |  
QY 393 TTGGCTTCGGAGTCAACCATGGGAGTGACGTCGGCAGGCGCATCTCTGGAGCCACATGA 452  
| | | | | | | | | | | | | | | | | |  
Db 179 GGGGCTTAGGTGTTGCCTTAGCCGTTTACCTTACTGCGGGTACTCTGGTGTCACTCA 238  
| | | | | | | | | | | | | | | | | |  
QY 453 ACGCAGCTGTGACCTTTGCTAACTGTGCGCTGGGCGCGCTGCCCTGGAGGAAAGTTTCCGG 512  
| | | | | | | | | | | | | | | | | |  
Db 239 ACCGGCGGTACAGTCGCAATCTGTTGTTGTTGCGTGTCTTGAACGTAAAAAGTTATCC 298  
| | | | | | | | | | | | | | | | | |  
QY 513 TCTATGTGCTGGGCGAGTTCTTGGGCTCTTCTGGGCGCTGCCACCATCTACAGTCTCT 572  
| | | | | | | | | | | | | | | | | |  
Db 299 CTTATATTGTTGCACAAATGTTAGGTGTTTTCGCGCGCTGTTGTGTACTTATGT 358  
| | | | | | | | | | | | | | | | | |  
QY 573 TCTACACGGCCATTCTCCACTTTTCGGGTGGAGCAGCTGATGGTGACCGGTCC----- 624  
| | | | | | | | | | | | | | | | | |  
Db 359 ATTACAATTTTATTATCGACTACGAAACAGGTCAACGGAAATTGTACGAGGATCACAAGAA 418  
| | | | | | | | | | | | | | | | | |  
QY 625 -CGTCGCTACAGCTGGCATTTTTCGACCTACCTTCTGATCAGATGACATTTGGGCGGG 683  
| | | | | | | | | | | | | | | | | |  
Db 419 GCCTCTTTACTGCGGGCGTCTTCTCTACTTACCCAGCAGCCCAAAATCTCTGTGATCCACG 478  
| | | | | | | | | | | | | | | | | |  
QY 684 GCTTCTGAATGAGCGGTGGTGACCGGATGTCAGCTGTGTCTCTTCGCCATCAGCG 743  
| | | | | | | | | | | | | | | | | |  
Db 479 CATTTTTCGAAAGTAAATTAATGCGGCTTATTCTCGTTGGCTTAATTTTAGCCTTAACAG 538  
| | | | | | | | | | | | | | | | | |  
QY 744 ACCAGGAGAAACACCCAGCAGTCCAGGAAACAGAGCGGCTGGTGATAGGCATCTCTGTTG 803  
| | | | | | | | | | | | | | | | | |  
Db 539 ATGATGTTAACGGGTGATACCTCGTGGGCTTTTAGGCCCATTAATTATCGGTATTTCTGATTG 598  
| | | | | | | | | | | | | | | | | |  
QY 804 TCATCATCGGGGTGTCCCTTGGCATGAACACAGGATATGCCATCAACCCGTCCTCCGGGACC 863  
| | | | | | | | | | | | | | | | | |  
Db 599 CGGTATCGGTGGTGCATTTGGGCCCATTAACCTGGAATTCGCTTAAACCCCTGCCCGGTGATT 658  
| | | | | | | | | | | | | | | | | |  
QY 864 TGCCCCCCCCGATCTTTCACCTTCATTTGTTGGGCGAAACAGGTCTTTCAGCAATGGGG 923  
| | | | | | | | | | | | | | | | | |  
Db 659 TTGGGCGCAAAATAGTCGCAATTTTTCGCGGATGGGGTGATATTGCTTTAACAGGTGGAC 718  
| | | | | | | | | | | | | | | | | |  
QY 924 AGAAC-----TGGTGGTGGGTGGCGAGTGGTGCCAGCCACCTTCTGGGTGCCCTATCTAGGTG 977  
| | | | | | | | | | | | | | | | | |  
Db 719 GCGATATTCTTTATTTCTTAGTCCCACTCAATGCTCCAAATGATTGGGGGTATTTTAGGCG 778  
| | | | | | | | | | | | | | | | | |  
QY 978 GCATCATCTACCTGGTCTTTCATTTGGGCTCCACCATCCACGGGAGCCCTTGAAATTTGGA 1035  
| | | | | | | | | | | | | | | | | |



Db 11954 AGCTGTTTCTCGATCTTGAACAGAGTCAGCATATCGTGGCGGCACTGCCGCCAGTCTTA 12013  
QY 633 ---CAGCTGGCATTTTGGCCACCTACCTTCCCTGATCACATGACATTTGTGGGGGGCTTCC 689  
Db 12014 ACCTGGCCGGGGTCTTTTCCACGTACCCGCATCCACATATCACTTTTATACAAGCGTTTG 12073  
QY 690 TGAATGAGGCGTGGCTGACCGGGATGCTCCAGCTGTGTCTCTTTCGCCATCACGGACCAGG 749  
Db 12074 CCGTGGAGACCAACCATCACGGCAATCCTGATGGCGATGATCATGGCCCTGACCGACGACG 12133  
QY 750 AGAAC 754  
Db 12134 GCAAC 12138

RESULT 14  
US-08-969-683A-19  
; Sequence 19, Application US/08969683A  
; Patent No. 6136576  
; GENERAL INFORMATION:  
; APPLICANT: GENENCOR INTERNATIONAL, INC.  
; TITLE OF INVENTION: METHOD FOR THE RECOMBINANT  
; TITLE OF INVENTION: PRODUCTION OF 1,3 PROPANEDIOL  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genencor International, Inc.  
; STREET: 4 Cambridge Place  
; CITY: Rochester  
; STATE: NY  
; COUNTRY: U.S.A  
; ZIP: 14618

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSEQ for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/969,683A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/20873  
FILING DATE: 13-NOV-1997  
APPLICATION NUMBER: 60/030,601  
FILING DATE: 13-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Glaiter, Debra  
REGISTRATION NUMBER: 33,888  
REFERENCE/DOCKET NUMBER: GC 369-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-864-7620  
TELEFAX: 650-845-6504  
TELEX:

INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12145 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: PHK28-26  
US-08-969-683A-19

Query Match 5.7%; Score 71.4; DB 3; Length 12145;  
Best Local Similarity 48.5%; Pred. No. 2.7e-11;  
Matches 235; Conservative 0; Mismatches 241; Indels 9; Gaps 1;  
QY 279 AGTTCCTGGCCGAGTTCATGAGCACATATGTCATGATGGTATTCGGCCTTGGTTCCGTGG 338  
Db 11654 AGTGGTGGCCGAGTTCTTGGCACCGGATGCTCATTTTCTTCGGCGCGGGCTGGCTCG 11713

QY 339 CCCATATGGTTCTAAATAAAAAATAATGGAGAGTACCTTGGTGTCAACTTGGGTTTGGCT 398  
Db 11714 CTGCGCTGCGGGTTCGCCGGGGCCAGCTTTGGTTCAGTGGGAGATCAGTATTATCTGGGCC 11773  
QY 399 TCGGAGTCACCATGGGAGTGCACGTGGCAGGCCGATCTCTGGAGCCCCACATGAACGCAG 458  
Db 11774 TTGGCGTCGCCATGGCCATCTACCTGACGGCCGGTGTCTCCGGCGCGCACCTAAATCCGG 11833  
QY 459 CTGTGACCTTTGTAACTGTGCGCTGGCGCGCTGCCCTGGAGGAAAGTTTCCGGTCTATG 518  
Db 11834 CCGTGACCATTGCCCTGTGGCTGTTCGCCCTGTTTGAACGCCGCAAGGTGCTGCCGTTTA 11893  
QY 519 TGCTGGGCGAGTTCTTGGGCTCCTTCTGGCGGCTGCCACCATCTACAGTCTCTTCTACA 578  
Db 11894 TTGTTGCCAGACGGCCGGGGCCTTCTGCGCGCGCGCTGGTGTATGGGCTCTATCGCC 11953  
QY 579 CGGCCATTCTCCACATTTTTCGGGTGGACAGTGGTGAACCGGTCCCGTCCGCTA----- 632  
Db 11954 AGCTGTTTCTCGATCTTGAACAGAGTCAGCATATCGTGGCGGCACTGCCGCCAGTCTTA 12013  
QY 633 ---CAGCTGCATTTTGGCCACCTACCTTCTGATCACATGACATTTGTGGGGGGCTTCC 689  
Db 12014 ACCTGGCCGGGGTCTTTTCCACGTACCCGCATCCACATATCACTTTTATACAAGCGTTTG 12073  
QY 690 TGAATGAGGCGTGGCTGACCGGGATGCTCCAGCTGTGTCTTTCGCCATCACGGACCAGG 749  
Db 12074 CCGTGGAGACCAACCATCACGCAATCCTGATGGCGATGATCATGGCCCTGACCGACGACG 12133  
QY 750 AGAAC 754  
Db 12134 GCAAC 12138

RESULT 15  
US-09-369-796-1  
; Sequence 1, Application US/09369796  
; Patent No. 6428767  
; GENERAL INFORMATION:  
; APPLICANT: BURCH, ROBERT R.  
; APPLICANT: DORSCH, ROBERT R.  
; APPLICANT: LAFFEND, LISA ANNE  
; APPLICANT: NAGARAJAN, VASANTHA  
; APPLICANT: NAKAMURA, CHARLES  
; TITLE OF INVENTION: 1,3-PROPANEDIOL AND POLYMER DERIVATIVES FROM A  
; TITLE OF INVENTION: FERMENTABLE CARBON SOURCE  
; FILE REFERENCE: CR-9715-F  
; CURRENT APPLICATION NUMBER: US/09/369,796  
; CURRENT FILING DATE: 1999-08-06  
; EARLIER APPLICATION NUMBER: 08/440,293  
; EARLIER FILING DATE: May 12, 1995  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 1  
; LENGTH: 12145  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-09-369-796-1

Query Match 5.7%; Score 71.4; DB 4; Length 12145;  
Best Local Similarity 48.5%; Pred. No. 2.7e-11;  
Matches 235; Conservative 0; Mismatches 241; Indels 9; Gaps 1;  
QY 279 AGTTCCTGGCCGAGTTCATGAGCACATATGTCATGATGGTATTCGGCCTTGGTTCCGTGG 338  
Db 11654 AGTGGTGGCCGAGTTCTTGGCACCGGATGCTCATTTTCTTCGGCGCGGGCTGGCTCG 11713  
QY 339 CCCATATGGTTCTAAATAAAAAATAATGGAGAGTACCTTGGTGTCAACTTGGGTTTGGCT 398  
Db 11714 CTGCGCTGCGGGTTCGCCGGGGCCAGCTTTGGTTCAGTGGGAGATCAGTATTATCTGGGCC 11773  
QY 399 TCGGAGTCACCATGGGAGTGCACGTGGCAGGCCGATCTCTGGAGCCCCACATGAACGCAG 458  
Db 11774 TTGGCGTCGCCATGGCCATCTACTGACGGCCGGTGTCTCCGGCGCGCACCTAAATCCGG 11833







GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model  
Run on: February 19, 2004, 19:52:52 ; Search time 512 Seconds  
(without alignments)  
8603.650 Million cell updates/sec

Title: US-09-849-980B-2  
Perfect score: 1258  
Sequence: 1 GGCTCTGGACTGGGACACA.....AGCAAGGCTTGTCGACAAA 1258

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2308684 seqs, 1750822206 residues

Total number of hits satisfying chosen parameters: 4617368

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
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- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1258	100.0	1258	9	US-09-849-980B-2
2	1258	100.0	1258	9	US-09-954-531-1344
3	963.2	76.6	1066	15	US-10-093-463-173
4	326.6	26.0	3757	15	US-10-094-749-545
5	260.8	20.7	1446	14	US-10-177-293-11
6	260.4	20.7	588	14	US-10-029-386-873
7	260.4	20.7	1599	14	US-10-177-293-9
8	216.4	17.2	1495	9	US-09-917-800A-1718
9	215	17.1	260	15	US-10-242-535A-5242
10	213.6	17.0	1532	9	US-09-822-830A-415
11	202.8	16.1	578	14	US-10-029-386-1382
12	166.6	13.2	181	14	US-10-029-386-15084
13	166.4	13.2	176	14	US-10-029-386-14576
14	132	10.5	843	14	US-10-156-761-7179
15	132	10.5	9025608	14	US-10-156-761-1

16	125.4	10.0	849	12	US-10-282-122A-31407	Sequence 31407, A
17	124.2	9.9	840	12	US-10-282-122A-30312	Sequence 30312, A
18	123.8	9.8	849	12	US-10-282-122A-23195	Sequence 23195, A
19	121	9.6	373	15	US-10-027-632-285939	Sequence 285939, A
20	111	8.8	843	12	US-10-282-122A-20129	Sequence 20129, A
21	110.6	8.8	846	12	US-10-282-122A-6642	Sequence 6642, Ap
22	108	8.6	385	10	US-09-918-995-36840	Sequence 36840, A
23	107.6	8.6	846	12	US-10-282-122A-39821	Sequence 39821, A
24	101.2	8.0	855	12	US-10-282-122A-33738	Sequence 33738, A
25	81.8	6.5	849	12	US-10-282-122A-36802	Sequence 36802, A
26	80	6.4	849	12	US-10-282-122A-41919	Sequence 41919, A
27	76.8	6.1	370	10	US-09-918-995-30179	Sequence 30179, A
28	76.8	6.1	813	12	US-10-282-122A-32762	Sequence 32762, A
29	72.4	5.8	1003	12	US-10-424-599-117118	Sequence 117118, A
30	71.4	5.7	12145	10	US-09-308-207-19	Sequence 19, Appl
31	71.4	5.7	12145	14	US-10-213-203-1	Sequence 1, Appli
32	71.4	5.7	12145	14	US-10-277-249-1	Sequence 1, Appli
33	71.4	5.7	12145	15	US-10-374-366-32	Sequence 32, Appl
34	70.6	5.6	1424	12	US-10-424-599-59520	Sequence 59520, A
35	70.2	5.6	789	12	US-10-282-122A-31114	Sequence 31114, A
36	70.2	5.6	9025608	14	US-10-156-761-1	Sequence 1, Appli
37	69.8	5.5	104	9	US-09-728-445-857	Sequence 857, App
38	69.4	5.5	747	14	US-10-156-761-6942	Sequence 6942, Ap
39	67.4	5.4	561	15	US-10-027-632-264839	Sequence 264839, A
40	67.4	5.4	561	15	US-10-027-632-264840	Sequence 264840, A
41	65	5.2	368	9	US-09-960-352-6096	Sequence 6096, Ap
42	62.6	5.0	3186778	15	US-10-027-632-174961	Sequence 174961, A
43	62.4	5.0	395	9	US-09-867-550-281	Sequence 281, App
44	60.6	4.8	795	12	US-10-282-122A-22079	Sequence 22079, A
45	60.6	4.8	1830121	14	US-10-329-960-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-849-980B-2  
; Sequence 2, Application US/09849980B  
; Patent No. US20020123611A1  
; GENERAL INFORMATION:  
; APPLICANT: SANTEN PHARMACEUTICAL CO., LTD.  
; TITLE OF INVENTION: No. US20020123611A1 Polypeptide Having Water Channel  
; TITLE OF INVENTION: Activity and DNA sequence  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SANTEN PHARMACEUTICAL CO., LTD.  
; STREET: 9 19 Shimoshinjo 3-chome Higashiyodogawa-Ku  
; CITY: Osaka  
; STATE: Osaka  
; COUNTRY: JAPAN  
; ZIP: 533-0021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB, storage  
; COMPUTER: IBM PS/2 or compatibles  
; OPERATING SYSTEM: WINDOWS 95/97  
; SOFTWARE: Microsoft Word 97  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/849,980B  
; FILING DATE: 19-OCT-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP98/01371  
; FILING DATE: 27-MAR-1998  
; APPLICATION NUMBER: JP 09-094845  
; FILING DATE: 28-MAR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Burton A. Amernick  
; REGISTRATION NUMBER: 24852  
; REFERENCE/DOCKET NUMBER: 1581/00156  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)331-7111  
; TELEFAX: (202)293-6229  
; INFORMATION FOR SEQ ID NO: 2:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1258 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: fat tissue
; FEATURE:
; NAME/KEY: exon
; LOCATION: F173..1198
; IDENTIFICATION METHOD: by experiment
US-09-849-980B-2

Query Match      100.0%; Score 1258; DB 9; Length 1258;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTCTGGACTGGGGACACAGGGATAGCTGAGCCCCAGCTGGGGGTGGAAGCTGAGCCAG 60
Db 1 GGCTCTGGACTGGGGACACAGGGATAGCTGAGCCCCAGCTGGGGGTGGAAGCTGAGCCAG 60

QY 61 GGACAGTCACGGAGGAACAAGATCAAGATCGCTGTAACTGAGAGCCCCCAAGCGGAG 120
Db 61 GGACAGTCACGGAGGAACAAGATCAAGATCGCTGTAACTGAGAGCCCCCAAGCGGAG 120

QY 121 GCTGAGAATCAGAGACATTTTCAGAGACATCTACAAATCTGAAAGACAAAACATGTTCA 180
Db 121 GCTGAGAATCAGAGACATTTTCAGAGACATCTACAAATCTGAAAGACAAAACATGTTCA 180

QY 181 AGCATCCGGGCACAGCGGTCCACCCGTGGTCCAAAATGGTCTCCTGGTCCGTGATAGC 240
Db 181 AGCATCCGGGCACAGCGGTCCACCCGTGGTCCAAAATGGTCTCCTGGTCCGTGATAGC 240

QY 241 AAAGATCCAGGAATACTGCAGAGGAAGATGGTGCAGAGATTCCTGGCCGAGTTCATGAG 300
Db 241 AAAGATCCAGGAATACTGCAGAGGAAGATGGTGCAGAGATTCCTGGCCGAGTTCATGAG 300

QY 301 CACATATGTATGATGGTATTCGGCTTGGTCCGGTCCGAGCCCATATGTTCTAAATAAAAA 360
Db 301 CACATATGTATGATGGTATTCGGCTTGGTCCGGTCCGAGCCCATATGTTCTAAATAAAAA 360

QY 361 ATATGGAGACTACCTTGGTGTCAACTTGGGTTTGGCTTCGGAGTCACCATGGAGTGCA 420
Db 361 ATATGGAGACTACCTTGGTGTCAACTTGGGTTTGGCTTCGGAGTCACCATGGAGTGCA 420

QY 421 CGTGGAGCCCGCATCTCTGGAGCCACATGAACGAGCTGTGACCTTTGTAACGTGC 480
Db 421 CGTGGAGCCCGCATCTCTGGAGCCACATGAACGAGCTGTGACCTTTGTAACGTGC 480

QY 481 GCTGGCCCGCGTCCCTGGAGGAAGTTTCCGGTCTATGTCTGGGGCAGTTCTCGGCTC 540
Db 481 GCTGGCCCGCGTCCCTGGAGGAAGTTTCCGGTCTATGTCTGGGGCAGTTCTCGGCTC 540

QY 541 CTTCTGGCGGCTGCCACCATCTACAGTCTCTTACACGGCCATTTTCCACCTTTTCGGG 600
Db 541 CTTCTGGCGGCTGCCACCATCTACAGTCTCTTACACGGCCATTTTCCACCTTTTCGGG 600

QY 601 TGGACAGCTGATGGTGACCGGTCCCGTCGCTACAGCTGGCATTTTTCACCTACCTTCC 660
Db 601 TGGACAGCTGATGGTGACCGGTCCCGTCGCTACAGCTGGCATTTTTCACCTACCTTCC 660

QY 661 TGATCAGATGACATTTCTGGCGGGCTTCTGAATGAGGCGTGGCTGACCGGGATGCTCCA 720
Db 661 TGATCAGATGACATTTCTGGCGGGCTTCTGAATGAGGCGTGGCTGACCGGGATGCTCCA 720

QY 721 GCTGTGTCTCTTCGCCATCAGGACCGAGAGAACACCCAGCACTGCCAGGAACAGAGGC 780
Db 721 GCTGTGTCTCTTCGCCATCAGGACCGAGAGAACACCCAGCACTGCCAGGAACAGAGGC 780

QY 781 GCTGTGTATAGGCATCCTCGTGGTCAATCATCGGGGTGTCCTTGGCATGAACACAGGATA 840
Db 781 GCTGTGTATAGGCATCCTCGTGGTCAATCATCGGGGTGTCCTTGGCATGAACACAGGATA 840
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Db 781 GCTGTGTATAGGCATCCTCGTGGTCAATCATCGGGGTGTCCTTGGCATGAACACAGGATA 840
QY 841 TGCCATCAACCCGTCCTGGGACCTGCCCCCGCATCTTACACCTTCACTTGTGTTGGG 900
Db 841 TGCCATCAACCCGTCCTGGGACCTGCCCCCGCATCTTACACCTTCACTTGTGTTGGG 900
QY 901 CAAACAGGTCTTTCAGCAATGGGGAGAACTGGTGGGTGCCAGTGGTGCCACCACTTCT 960
Db 901 CAAACAGGTCTTTCAGCAATGGGGAGAACTGGTGGGTGCCAGTGGTGCCACCACTTCT 960
QY 961 GGTGCTCTATCTAGGTGGCATCTACCTGGTCTTCACTGGTCCACCATCCACGGGA 1020
Db 961 GGTGCTCTATCTAGGTGGCATCTACCTGGTCTTCACTGGTCCACCATCCACGGGA 1020
QY 1021 GCCCTGAAATTCGAGGATTCCTGGCGGTATGAAGACCAACCGGATAAACCCTATTGCCAA 1080
Db 1021 GCCCTGAAATTCGAGGATTCCTGGCGGTATGAAGACCAACCGGATAAACCCTATTGCCAA 1080
QY 1081 GATGGGATCTCATGAACCCACGATCTCTCCCTCACCCCGTCTCTGTGAGCCCTGCA 1140
Db 1081 GATGGGATCTCATGAACCCACGATCTCTCCCTCACCCCGTCTCTGTGAGCCCTGCA 1140
QY 1141 CAGATCTTCAGTCCACCTGCCCCACCTTACATGAATCCATGGCCCTAGAGCACTTCTA 1200
Db 1141 CAGATCTTCAGTCCACCTGCCCCACCTTACATGAATCCATGGCCCTAGAGCACTTCTA 1200
QY 1201 AGCAGAGATTTATTTGTGATCCCATCCATTTCCCAATAAAGCAAGGCTTGTCCGACAAA 1258
Db 1201 AGCAGAGATTTATTTGTGATCCCATCCATTTCCCAATAAAGCAAGGCTTGTCCGACAAA 1258
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RESULT 2

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US-09-954-531-1344
; Sequence 1344, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cance
; FILE REFERENCE: 689290-77
; CURRENT APPLICATION NUMBER: US/09/954,531
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1344
; LENGTH: 1258
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-531-1344
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Query Match      100.0%; Score 1258; DB 9; Length 1258;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTCTGGACTGGGGACACAGGGATAGCTGAGCCCCAGCTGGGGGTGGAAGCTGAGCCAG 60
Db 1 GGCTCTGGACTGGGGACACAGGGATAGCTGAGCCCCAGCTGGGGGTGGAAGCTGAGCCAG 60

QY 61 GGAAGAGTCACGGAGGAACAAGATCAAGATGCGTGTAACTGAGAGCCCCCAAGCGGAG 120
Db 61 GGAAGAGTCACGGAGGAACAAGATCAAGATGCGTGTAACTGAGAGCCCCCAAGCGGAG 120

QY 121 GCTGAGAATCAGAGACATTTTCAGAGACATCTACAAATCTGAAAGACAAAACATGTTCA 180
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*Good date*







Db 1133 AAATGGAGACTCTGTGGGTATGAAGACACGGGATAACCGTATTGCCAAGATGGA 1192  
Qy 1088 TCTCATGAACCCACGATCTCTCCCTCACCCCCGTCTCTGTGAGCCCTGCAACAGATCT 1147  
Db 1193 TCTCATGAACCCATGATCTCTCCCTCACCCCTCATCTCGTGAGCCTTGCAACAGATCT 1252  
Qy 1148 TCAGTCCACCTGCCCCACCCCTTACATGAATCCATGGCCCTAGAGCACTTCTAAGCAGAG 1207  
Db 1253 TCAGTCCACTCTGCCCCACCCCTTACATGAATCCATGGCCCTAGAGCACTTCTAAGCAGAG 1312  
Qy 1208 ATTATTTGTGATCCCATCCATCCATTTCCCCAATAAAGCAAGGCTTGTCCGACA 1256  
Db 1313 ATTATTTGTGATCCCATCCCTTCCCCAATAAAGCAAGCTTGTCCCA 1361

RESULT 5  
US-10-177-293-11  
; Sequence 11, Application US/10177293  
; Publication No. US20030124128A1  
; GENERAL INFORMATION:  
; APPLICANT: Lillie, James  
; APPLICANT: Glatt, Karen  
; APPLICANT: Zhao, Xumei  
; APPLICANT: Gannavarpu, Manjula  
; APPLICANT: Kamatkar, Shubhangi  
; APPLICANT: Mertens, Maureen  
; APPLICANT: Myer, Vic  
; APPLICANT: Wang, Youzhen  
; APPLICANT: Xu, Yongyao  
; APPLICANT: Hoersch, Sebastian  
; APPLICANT: Monahan, John  
; APPLICANT: Meyers, Rachel E.  
; APPLICANT: Bast Jr., Robert C.  
; APPLICANT: Hortobagyi, Gabriel N.  
; APPLICANT: Pusztai, Lajos  
; APPLICANT: Meric, Funda  
; APPLICANT: Sahin, Aysegul  
; APPLICANT: Mills, Gordon B.  
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,  
; TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER  
; FILE REFERENCE: MRI-038  
; CURRENT APPLICATION NUMBER: US/10/177,293  
; CURRENT FILING DATE: 2002-06-21  
; PRIOR APPLICATION NUMBER: US 60/299,887  
; PRIOR FILING DATE: 2001-06-21  
; PRIOR APPLICATION NUMBER: US 60/301,572  
; PRIOR FILING DATE: 2001-06-27  
; PRIOR APPLICATION NUMBER: US 60/306,501  
; PRIOR FILING DATE: 2001-07-18  
; PRIOR APPLICATION NUMBER: US 60/325,002  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US 60/362,585  
; PRIOR FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx  
; PRIOR FILING DATE: 2002-05-14  
; NUMBER OF SEQ ID NOS: 506  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 1446  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-10-177-293-11  
Query Match 20.7%; Score 260.8; DB 14; Length 1446;  
Best Local Similarity 58.8%; Pred. No. 5e-73;  
Matches 470; Conservative 0; Mismatches 327; Indels 3; Gaps 1;  
Qy 268 GATGGTGGAGAGTTCTTGGCGAGTTTCATGAGCACATATGTCATGATGGTATTCGGCCT 327  
Db 124 GTTGCTCCGACAGGCGTGGCGAGTGCCTGGGACCCCTCATCTCGTGTGATGTTGGCTG 183  
Qy 328 TGGTTCGTCGCCCCCATATGGTTCTAAATAA---AAATATGGGAGCTACCTTGGTGTCAA 384

Db 184 TGGCTCGTGGCCCAAGTTGTGCTCAGCCGGGCAACCCACGGTGGTTCTCTCACCATCAA 243  
Qy 385 CTTGGGTTTTGGCTTCGGAGTCACCATGGGAGTGACGTGGCAGGCCGATCTCTGGAGC 444  
Db 244 CCTGGCCTTTGGCTTGTGCTGCTCACTCTGGGCATCCTCATCGCTGGCCAGGTCTCTGGGGC 303  
Qy 445 CCACATGAACGCAGCTGTGACCTTTTGCTAACTGTGCGTGGCCCGCGTGCCTCGGAGGAA 504  
Db 304 CCACCTGAACCCCTGCCGTGACCTTTGGCATGTGCTTCTGGCTCGTGAGCCCTGGATCAA 363  
Qy 505 GTTTCGGGTCTATGTGCTGGGGCAGTTCTCTGGGCTCCTTCTGGCGGTGCCACCATCTA 564  
Db 364 GCTGCCCATCTACACCTGGCACAGACGCTGGAGCCTTCTTGGGTGCTGGAATAGTTT 423  
Qy 565 CAGTCTCTTCTACACGGCCATTCTCCACTTTTCGGGTGGACAGCTGATGGTGACCGGTCC 624  
Db 424 TGGGCTGTATTATGATGCAATCTGGCACTTTGCCGACAACAGCTTTTGTTCGGGCC 483  
Qy 625 CGTCGCTACAGCTGGCATTTTGGCCACCTACCTTCCCTGATCAGATGATGATGTTGGCGGG 684  
Db 484 CAATGGCACAGCCGGCATCTTTGCTACTACCTACCCCTCTGGACACTTGGATATGATCAATGG 543  
Qy 685 CTTCTCTGAATGAGGGCTGGCTGACCGGGATGCTCCAGCTGTGTCTCTTCGCCCATCACGGA 744  
Db 544 CTTCTTTGACCACTTATAGGCACAGCCTCCCTTATCGTGTGTGTGCTGGCCATTGTTGA 603  
Qy 745 CCAGGAGAAACAAACCCAGCACTGCCAGAAACAGAGGCGCTGGTATAGGCATCCTCGTGT 804  
Db 604 CCCTTACAAACCCCGTCCCCGAGGCTGGAGGCTTACCGTGGGCTGGTGGTCTCT 663  
Qy 805 CATCATCGGGGTGTCCCTTGGCATGAACACAGGATATGCCATCAACCCGTCCCGGACCT 864  
Db 664 GGTCAATGGCACCTCCATGGGCTTCAACTCCGGCTATGCCGTCAACCCCTGCCCGGACTT 723  
Qy 865 GCCCCCGCGCATCTTACCTTCACTGCTGTTGGGCAACAGGTCTTTCAGCAATGGGA 924  
Db 724 TGGCCCCCGCCTTTTACAGCCCTTTCGGGCTGGGCTCTGCAGTCTTACGACCGGCCA 783  
Qy 925 GAACCTGGTGGTGGTGCAGTGTGGCACCACCTTCTGGGTGCCATCTAGGTGGCATCAT 984  
Db 784 GCATTGGTGGTGGTGCCCATCGTGTCCCCACTCTCTGGGCTCCATTGGCGGTGTCTTCGT 843  
Qy 985 CTACCTGGTCTTTCATTGGCTCCACCATCCACGGGAGGCCCTTGAAATTTGGAGGATTCTGT 1044  
Db 844 GTACCAGCTGATGATCGCTGCCACCTGGAGCAGCCCCACCCCTCCAACGAGGAAGAGAA 903  
Qy 1045 GGCGTATGAAGACCACCGGA 1064  
Db 904 TGTGAAGCTGGCCCCATGTGA 923

RESULT 6  
US-10-029-386-873  
; Sequence 873, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GI  
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO  
; FILE REFERENCE: AEOMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 873  
; LENGTH: 588  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AL137070.3

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; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.81
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.94
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.55
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.65
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.72
; OTHER INFORMATION: SWISSPROT HIT: O14520, EVALUE 2.00e-43
; OTHER INFORMATION: NT HIT: gi14720872, EVALUE 0.00e+00
; OTHER INFORMATION: EST_HUMAN HIT: AI732264.1, EVALUE 0.00e+00
US-10-029-386-873

Query Match      20.7%; Score 260.4; DB 14; Length 588;
Best Local Similarity 96.0%; Pred. No. 4.5e-73;
Matches 267; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 908 GTCCTCAGCAATGGGAGAACTGGTGGTGGGTCGCCAGTGGTGGCACCACCTTCTGGGTGCC 967
Db 311 GCCTGACGGATGGGAGAACTGGTGGTGGGTCGCCAGTGGTGGCACCACCTTCTGGGTGCC 370

QY 968 TATCTAGTGGCATCATCTACCTGGTCTTCACTGGTCTCCACCATCCACGGGAGCCCCCTG 1027
Db 371 TCTCTAGTGGCATCATCTACCTGGTCTTCACTGGTCTCCACCATCCACGGGAGCCCCCTG 430

QY 1028 AAATTGAGGATCTGTGGCGTATGAAGACCACGGGATAACCGTATTGCCCAAGATGGGA 1087
Db 431 AAATTGAGGACTCTGTGGCGTATGAAGACCACGGGATAACCGTATTGCCCAAGATGGGA 490

QY 1088 TCTCATGAACCCACGATCTCTCCCTCACCCCGTCTCTGTGAGCCCTGCCAACAGATCT 1147
Db 491 TCTCATGAACCCACGATCTCTCCCTCACCCCGTCTCTGTGAGCCCTGCCAACAGATCT 550

QY 1148 TCAGTCCACCCCTGCCACCCTTACATGAATCCATGGC 1185
Db 551 TCAGTCCACTCTGCCACCCTTACATGAATCCATGGC 588

RESULT 7
US-10-177-293-9
; Sequence 9, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Pusztai, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
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; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1022, 1081
; OTHER INFORMATION: n = A,T,C or G
US-10-177-293-9

Query Match      20.7%; Score 260.4; DB 14; Length 1599;
Best Local Similarity 58.6%; Pred. No. 7e-73;
Matches 469; Conservative 1; Mismatches 327; Indels 3; Gaps 1;

QY 268 GATGGTCCGAGAGTTCTGCGCGAGTTTCATAGACACATATGTCATGATGATGATTCGGGCT 327
Db 124 GYTGCTCCGACAGGCGCTGGCGAGTGCTTGGGACCCCTCATCTCTCGTATGTTGGCTG 183

QY 328 TGGTTCGCTGGCCCATATGTTTCTAAATAAA---AAATATGGGAGCTACCTTGGTGTCAA 384
Db 184 TGGTTCGCTGGCCCATGTTGTCTCAGCCGGGACCCACGGTGGTTCCTCACCATCAA 243

QY 385 CTTGGGTTTTGGCTTCGGAGTCACCATGGGAGTGCACGTGGCAGGCCGTCATCTCTGGAGC 444
Db 244 CTTGGGCTTTGGCTTTGCTGTCACTCTGGGCACTCTCATCGCTGGCCAGGTCCTCTGGGGC 303

QY 445 CCACATGAACGACGCTGTGACCTTTGCTAACTGTGCGTGGGCGCGCTGCCCTGGAGGAA 504
Db 304 CCACCTGAACCCCTGCCGTGACCTTTGCCATGTGCTTCCTGGCTCGTGAGCCCTGGATCAA 363

QY 505 GTTTCGGTCTATGTGCTGGGCGAGTTCTTGGGCTCCTTCTTGGGCTGCCACCATCTA 564
Db 364 GCTGCCCATCTACACCCCTGGCACAGACGCTGGGAGCCTTCTTGGGTGCTGGAATAGTTTT 423

QY 565 CAGTCTCTTCTACACGGCCATCTCCACTTTTCGGGTGGACAGCTGATGGTACCGGTCC 624
Db 424 TGGGCTGTATTATGATGCAATCTGGCACACTTGGCCGACCAACCAAGCTTTTGTTCGGGGCC 483

QY 625 CGTCGCTACAGCTGGCATTTTTCACCTACCTACCTTCTGAGTGGGAGCTGATGGTGGGGG 684
Db 484 CAATGGCACAGCGCGCATCTTTGCTACCTACCTACCTCTGGACACTTGGATATGATCAATGG 543

QY 685 CTTCTGAATGAGGCGTGGCTGACCGGATGTCCAGCTGTGTCTCTTCGCCATCACGGA 744
Db 544 CTTCTTTGACCACTTATAGGACAGCCCTCCCTTATCGTGTGTGTCTGGCCATGTTGA 603

QY 745 CCAGGAGAACAAACCCAGCACTGCCAGGAACAGAGGCGCTGGTATAGGCATCCTCGTGGT 804
Db 604 CCCYTACAACAACCCCGTCCCGGAGGCTGGAGGCTTCACCGTGGGCTGGTGGTCTCT 663

QY 805 CATCATCGGGGTGTCCTTGGCATGAACACAGGATATGCCATCAACCCGTCCTCGGACCT 864
Db 664 GGTCAATTGGCACTCCATGGGCTTCAACTCCGCTATGCCGTCAACCCCTGCCCGGACTT 723

QY 865 GCGCCCGCGCATCTTCACTTTCATTTGCTGGTGGGCAACAGGCTCTTCAGCAATGGGA 924
Db 724 TGGCCCGCGCTTTTACAGCCCTTGGGCTGGGCTCTCGAGTCTTCACGACCGGCCA 783

QY 925 GAACTGGTGGGTGCCAGTGGTGGCACCCTTCTGGGTGCTATCTAGTGGCATCAT 984
Db 784 GCATTGGTGGGTGCCCATGTCCTCCCACTCTCTGGGCTCCATTGCGGGTGTCTTCGT 843

QY 985 CTACCTGGTCTTTCATTTGGCTCCACCATCCACGGGAGCCCTGAAATTTGGAGATCTGT 1044
Db 844 GTACCAGCTGATGATCGGCTGCCACCTGGAGCAGCCCCCACCTCCACGAGGAAGAA 903

QY 1045 GCGGTATGAAGACCACGGGA 1064
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QY 186 CCGGGCACAGCGGTCCACCCGTGGCTCCAAATGGTCTCCTGCTCCGTGATAGCAAAGA 245  
Db 181 CTGGGCACAGCGGTCCACCTGTGGCTCCAAATGGTCTCCCGTCCCTGATAGCAAAGA 240  
QY 246 TCC 248  
Db 241 TAC 243

RESULT 10  
US-09-822-830A-415  
; Sequence 415, Application US/09822830A  
; Patent No. US20020142952A1  
; GENERAL INFORMATION:  
; APPLICANT: Genetics Institute, Inc.  
; APPLICANT: Wong, Gordon G.  
; APPLICANT: Clark, Hilary  
; APPLICANT: Fechtel, Kim  
; APPLICANT: Agostino, Michael J.  
; APPLICANT: Howes, Steven H.  
; APPLICANT: Resnick, Richard J.  
; APPLICANT: Gulukota, Kamalakara  
; APPLICANT: Graham, James R.  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS  
; FILE REFERENCE: GIN 6402  
; CURRENT APPLICATION NUMBER: US/09/822,830A  
; PRIOR FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: 60/195,604  
; PRIOR FILING DATE: 2000-04-06  
; NUMBER OF SEQ ID NOS: 631  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 415  
; LENGTH: 1532  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-822-830A-415

Query Match 17.0%; Score 213.6; DB 9; Length 1532;  
Best Local Similarity 58.5%; Pred. No. 8.3e-58;  
Matches 372; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

QY 429 GCGCATCTCTGGAGCCACATGAACGCAGCTGTGACCTTTGCTAACTGTGCGTGGGCC 488  
Db 1 GCCAGGTCTCTGGGGCCACCTGAACCCCTGCCGTGACCTTTGCCATGTCTCCTGGCTC 60  
QY 489 GCGTCCCTGGAGGAAGTTTCCGGTCTATGTGTGGGGCAGTTCTCGGCTCCTCTCTGG 548  
Db 61 GTGAGCCCTGGATCAAGCTGCCATCTACACCCCTGGCACAGCTGGAGCCTTCTTGG 120  
QY 549 CGGTGCCACCATCTACAGTCTCTTACACGGGCATCTCCACTTTTCGGGTGGACAGC 608  
Db 121 GTGTGGAATAGTTTGGGCTGTATTATGATGAATCTGGCACTTGGCGACAAACAGC 180  
QY 609 TGATGGTGACCGGTCCCGTACAGCTGGCAATTTTGGCACTTACCTTCCCTGATCACA 668  
Db 181 TTTTGTTCGGGGCCCAATGGCACAGCCGGCATCTTTGCTACTACCTACCCCTCTGGAC 240  
QY 669 TGACATTGTGGCGGGCTTCTCTGAATGAGCGTGGCTGACCGGATGCTCCAGTGTGTC 728  
Db 241 TGGATATGATCAATGGCTTCTTTGACCAAGTTTATAGGCACAGCTCCCTTATCTGTGTG 300  
QY 729 TCTTCGCCATCACGGACCAGGAGAACACCCAGCACTGCCAGGAACAGAGCGCTGGTGA 788  
Db 301 TGCTGGCCATTGTTGACCCCTACACAAACCCCGTCCCGAGGCTTGAGGCTTCACCG 360  
QY 789 TAGGCATCCTCGTGGTCAATCGGGGTGTCCTTGGCATGAACACAGGATATGCCATCA 848  
Db 361 TGGGCTGTGGTCTGTGTCATTTGGCACCTCCATGGGCTTCAACTCCGGCTATGCCGTCA 420  
QY 849 ACCCGTCCCGGACCTGCCCCCGCATCTTCACTTCACTTGTGTTGGGGGAAACAGG 908  
Db 421 ACCCTGCCCGGACTTTGGCCCCCGCCTTTTACAGCCCTTTGCGGGCTGGGGCTCTGCAG 480

QY 909 TCTTCAGCAATGGGGAGAACTGGTGGTGCCAGTGGTGCCACCACTTCTGGGTGCCT 968  
Db 481 TCTTCAGCACCGGCCAGCAATTGGTGGTGCCCATCGTGTCCCCCACTCCTGGGTCCA 540  
QY 969 ATCTAGGTGGCATCATCTACCTGGTCTTCAATTGGCTCCACCATCCACGGGAGCCCTGA 1028  
Db 541 TTGCGGTGTCTTCTGTACCAAGCTGATGATCGGCTGCCACCTGGAGCAGCCCCCACCT 600  
QY 1029 AATTGGAGGATTCTGTGGCGTATGAAGACCACGGGA 1064  
Db 601 CCAACGAGGAAGAGAATGTGAAGCTGGCCCATGTGA 636

RESULT 11  
US-10-029-386-1382  
; Sequence 1382, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GE  
; FILE REFERENCE: AEOMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 1382  
; LENGTH: 578  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AL136317.2  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.7  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.1  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.9  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.5  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.3  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.8  
; OTHER INFORMATION: SWISSPROT HIT: O14520, EVALUE 2.00e-25  
; OTHER INFORMATION: EST\_HUMAN HIT: A1792403.1, EVALUE 0.00e+00  
; OTHER INFORMATION: NT HIT: gi14736665, EVALUE 1.00e-108  
US-10-029-386-1382

Query Match 16.1%; Score 202.8; DB 14; Length 578;  
Best Local Similarity 94.6%; Pred. No. 1.6e-54;  
Matches 210; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 694 TGAGGCGTGGCTGACCGGGATGCTCCAGCTGTGTCTTTCGCCATCACGGACGAGGAGAA 753  
Db 213 TCAGGAGTGGCTGACCGGGATGCTCCAGCTGTGTCTTTCGCCATCGTGGACGAGGAGAA 272  
QY 754 CAACCCAGCACTGCCAGGAACAGAGGCGCTGTGATAGGATCCTCGTGGTCAATCATCGG 813  
Db 273 CAACCCAGCACTGCCAGGAACACACGCACTGTGTGATAGGATCCTCGTGGTCAATCATCAG 332  
QY 814 GGTGTCCCTTGGCATGAACACAGGATATGCCATCAACCCGTCCTCCGGGACCTGCCCCCCCG 873  
Db 333 GGTGTACCATGGCATGAACACAGGATATGCCATCAATCCGTCCTCCGGGACCTGCCCCCCCG 392  
QY 874 CATCTTCACCTTCACTTGTGTGGGGGCAACAGGTCTTTCAG 915  
Db 393 CATCTTCACCTTCACTTGTGTGGGGGCAACAGGTCTTTCAG 434

RESULT 12  
US-10-029-386-15084  
; Sequence 15084, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.



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; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 15084
; LENGTH: 181
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL136317.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.8
; OTHER INFORMATION: SWISSPROT HIT: O14520, EVALUE 2.00e-18
; OTHER INFORMATION: EST HUMAN HIT: AW967265.1, EVALUE 1.00e-80
; OTHER INFORMATION: NT HIT: g114736665, EVALUE 5.00e-85
US-10-029-386-15084

Query Match      13.2%; Score 166.6; DB 14; Length 181;
Best Local Similarity 95.0%; Pred. No. 4.5e-43;
Matches 172; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 713 ATGCTCCAGTGTGTCTCTTCGCCCATCAGGACCCAGGAGAACACCCAGCACTGCCAGGA 772
Db 1 ATGCTCCAGTGTGTCTCTTCGCCCATCGTGACCCAGGAGAACACCCAGCACTGCCAGGA 60

Qy 773 ACAGAGCGGTGGTGATAGGCATCTCTCGGTGCATCATCGGGGTGTCCTTGGCATGAAC 832
Db 61 ACACAGCACTGGTGATAGGCATCTCTCGGTGCATCATCAGGGGTGTACCATGGCATGAAC 120

Qy 833 ACAGGATATGCCATCAACCCGTCGCGGACTGCCCCCGCATCTTCACTTCAATGCT 892
Db 121 ACAGGATATGCCATCAATCCGTCGCGGACTGCCCCCGCATCTTCACTTCAATGCT 180

Qy 893 G 893
Db 181 G 181

RESULT 13
US-10-029-386-14576
; Sequence 14576, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 14576
; LENGTH: 176
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL137070.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.81
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.94
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.55
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; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.65
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.72
; OTHER INFORMATION: EST HUMAN HIT: AA295848.1, EVALUE 7.00e-85
; OTHER INFORMATION: NT HIT: g114720872, EVALUE 1.00e-94
; OTHER INFORMATION: SWISSPROT HIT: O14520, EVALUE 1.00e-24
US-10-029-386-14576

Query Match      13.2%; Score 166.4; DB 14; Length 176;
Best Local Similarity 96.6%; Pred. No. 5.1e-43;
Matches 170; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 975 GTGGCATCATCTACCTGGTCTTTCATTGGCTCCACCATCCACGGGAGCCCTGAAATGG 1034
Db 1 GTGGCATCATCTACCTGGTCTTTCATTGGCTCCACCATCCACGGGAGCCCTGAAATGG 60

Qy 1035 AGGATTCTGTGGCGTATGAAGACCACGGGATAAACCGTATTGCCCAAGATGGGATCTCATG 1094
Db 61 AGGACTCTGTGGCGTATGAAGACCACGGGATAAACCGTATTGCCCAAGATGGGATCTCATG 120

Qy 1095 AACCCACGATCTCTCCCTCACCCCGCTCTCTGTGAGCCCTGCCAACAGATCTTCA 1150
Db 121 AACCCATGATCTCTCCCTCACCCCTCATCTCCGTGAGCCTTGCCAACAGATCTTCA 176

RESULT 14
US-10-156-761-7179
; Sequence 7179, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 7179
; LENGTH: 843
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(843)
US-10-156-761-7179

Query Match      10.5%; Score 132; DB 14; Length 843;
Best Local Similarity 51.1%; Pred. No. 1.3e-31;
Matches 337; Conservative 0; Mismatches 320; Indels 3; Gaps 1;

Qy 365 GGGAGCTACCTTGGTGTCAACTTGGGTTTGGCTTCGGAGTCACCATGGGAGTGCACGTG 424
Db 145 GGAACACGACGACGATCGGCTGGGCTGGGTCATCGGGTCACCATGGGCGTGTATGTC 204

Qy 425 GCAGGCGCATCTCTGGAGCCCCACATGAACGACGCTGTGACCTTTGCTAACTGTGGCTG 484
Db 205 GCGGCGCGCTGAGCGGTGCGCATCTCAACCCCGCGGTGACGGTCACTCTCGCCGCTTC 264

Qy 485 GGCCGCGTCCCTGGAGGAAGTTTCCGGTCTATGTGTGGGGCAGTTCTGTGGCTCCTTC 544
Db 265 AAGGGTTTCCCGTGGAGCAAGGTTCGCCCTTACGCGGTGGCCACGACGCTCGGCGCTTC 324

Qy 545 CTGGCGGCTGCCACCATCTACAGTCTCTTCTTACACGGGCATTTCTCCACTTTTCGGGTGA 604
Db 325 GTGGCGGCTCTCTCGTGGCTGGAACTACACCGAGCGCTGGCGAAGCCGACCCCGGC 384
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QY 605 CAGCTGATGGTACCGGTCCCGTCGCTACAGCTGGCATTTTTCACACCTACCTTCCTGAT 664  
Db 385 CACACCTCAAGACGAGGGCGTGTCTCCACGCTCCCGCCCAACGGCAACCCGAACCTG 444  
QY 665 CACATGACATTGTGGCGGGCTTCCTGAATAGGCGTGGCTGACCGGGATGCTCCAGCTG 724  
Db 445 CCGGTCCACGAGTGGGGCGGTTCGCGCACAGGTATCGGTACCGCATCTCTCTGCTG 504  
QY 725 TGTCTCTTCGCCATCACGGACAGGAGAAACACCCAGCACTGCCAGGAACAGAGGCGCTG 784  
Db 505 CTGATCCTCGCCATCACGGACCTGTCTCAACACGCCCCCGGGCCAAACCTGGCCCCGTTT 564  
QY 785 GTGATAGGCATCCTCGTGTGTCATCATCGGGGTGTCCTTGGCATGAACACAGGATATGCC 844  
Db 565 ATCATCGGCGCTGGTGTGTCGTCGATCGGCATCGGCTGGGGCACCAACGCGGGCTACGCG 624  
QY 845 ATCAACCCGTCGCGGACCTGCCCGCCCGCATCTTCACTTCACTGCTGTTGGGGCA-- 902  
Db 625 ATCAACCCGGCACGCGACTTCGGTCCCCCGGCTGGCCAGCTTCAATCACGGGCTACGGCAGC 684  
QY 903 -AACAGGTCTTACGAATAGGGAGAACTGGTGGGTGCCAGTGGTGCCACCACTTCTG 961  
Db 685 GCATGGCGAGATCAGTACGGGAATTCTACTTCTGGGTGCCGATCATCGTCCGCTGATC 744  
QY 962 GGTGCCATATAGTGGCATCATCTACCTGCTTTCATTTGGTCCACCATCCACGGGAG 1021  
Db 745 GCGGCTGTCTCGCGGGGTGCTGTACAAGTTCTCTGTTGGGCGGTTCTTGGCCGACGCG 804

RESULT 15

US-10-156-761-1  
; Sequence 1, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 1  
; LENGTH: 9025608  
; TYPE: DNA  
; ORGANISM: Streptomyces avermitilis  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (418715)  
; OTHER INFORMATION: a, t, c, g, other or unknown  
US-10-156-761-1

Query Match 10.5%; Score 132; DB 14; Length 9025608;  
Best Local Similarity 51.1%; Pred. No. 7.9e-30;  
Matches 337; Conservative 0; Mismatches 320; Indels 3; Gaps 1;  
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QY 425 GCAGGCGCATCTCTGGAGCCCATGAACGCGAGTGTGACCTTGTAACTGTGCGCTG 484  
Db 8574521 GCGGCGGCTGAGCGGTGGGCATCTCAACCCCGCGGTGACGCTCACTCTCGCCGCGTTC 8574580

QY 485 GGCCGCGTGCCCTTGAGGAAGTTTCCGGTCTATATGTGTGGGCGAGTTCTTGGGCTCCTTC 544  
Db 8574581 AAGGGTTTCCCGTGGAGCAAGGTGCGGCCCTACCGGTGGCCCGAGACGCTCGGCGCCTTC 8574640  
QY 545 CTGGCGGCTGCCACCATCTACAGTCTCTTCTACACGGGCATTTCTCCATTTTTCGGGTGGA 604  
Db 8574641 GTGGCGGCGCTCTCTGTGCGCTGGAATACACCGAGGCGCTGGCGAAGGCCGACCCCGGC 8574700  
QY 605 CAGCTGATGGTGACCGGTCCCGTCGCTACAGCTGGCATTTTTCACACCTACCTTCTCTGAT 664  
Db 8574701 CACACCTCAAGACGACGAGGCGTGTCTCCACGCTCCCGCCAAACGGCAACCCGAACCTG 8574760  
QY 665 CACATGACATTGTGGCGGGCTTCTTGAATGAGGCGTGGGTGACCGGGATGCTCCAGCTG 724  
Db 8574761 CCGGTCCACGAGTGGGCGGTTCGCGACACAGGTCAATCGGTACCGCATCTCTCTGCTG 8574820  
QY 725 TGTCTCTTCGCCATCACGGACAGGAGAAACCCAGCACTGTCAGGAACAGAGGCGCTG 784  
Db 8574821 CTGATCCTCGCCATCACGGACCTGCTCAACACGCCCCCGGCGCAACCTTGGCCCCGTTT 8574880  
QY 785 GTGATAGGCATCCTCGTGTGTCATCATCGGGGTGTCCTTGGCATGAACACAGGATATGCC 844  
Db 8574881 ATCATCGGCGTGGTGTGTCGTCGCGATCGGCATGGCTGGGCGACCAACGCGGGCTACGCG 8574940  
QY 845 ATCAACCCGTCGCGGACCTGCCCGCCCGCATCTTCACTTCACTTGTGTTGGGGCA-- 902  
Db 8574941 ATCAACCCGCGACGCGACTTCGGTCCCCCGGTGGCCAGTTTCAATCACGGGCTACGGCAGC 8575000  
QY 903 -AACAGGTCTTACGCAATGGGAGAACTGGTGGGTGGTGCCAGTGGTGCCACCACTTCTG 961  
Db 8575001 GCATGGCGAGATCAGTACGGGAATTCTACTTCTGGGTGCCGATCATCGGTCCGCTGATC 8575060  
QY 962 GGTGCCATATAGGTGGCATCATCTACCTGCTTTCATTTGGCTCCACCATCCACGCGGAG 1021  
Db 8575061 GCGGCTGTCTCGGCGGGGTGCTGTACAAGTTCTTCTGTTGGGCGGTTCTCTGCGGACGCGC 8575120

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Job time : 3447 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 19, 2004, 21:06:08 ; Search time 590 Seconds  
(without alignments)  
122.397 Million cell updates/sec

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Perfect score: 1794  
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1794	100.0	342	9	US-09-849-980B-1 Sequence 1, Appli
2	1631	90.9	346	15	US-10-093-463-174 Sequence 174, App
3	702	39.1	292	14	US-10-177-293-10 Sequence 10, Appl
4	463.5	25.8	126	15	US-10-094-749-2184 Sequence 2184, Ap
5	432.5	24.1	281	14	US-10-156-761-14729 Sequence 14729, A
6	321.5	17.9	249	14	US-10-156-761-14492 Sequence 14492, A
7	308.5	17.2	264	14	US-10-156-761-14193 Sequence 14193, A
8	307.5	17.1	234	10	US-09-769-787-9 Sequence 9, Appli
9	269	15.0	58	14	US-10-029-386-27867 Sequence 27867, A
10	236.5	13.2	323	15	US-10-095-027-254 Sequence 254, App
11	226.5	12.6	265	14	US-10-097-340-12 Sequence 12, Appl
12	226.5	12.6	265	14	US-10-171-311-16 Sequence 16, Appl
13	200	11.1	107	9	US-09-867-550-282 Sequence 282, App
14	184	10.3	249	15	US-10-409-701-15 Sequence 15, Appl
15	184	10.3	249	15	US-10-310-154-606 Sequence 606, App

16	168	9.4	261	14	US-10-023-896-55	Sequence 55, Appl
17	168	9.4	261	14	US-10-023-896-84	Sequence 84, Appl
18	168	9.4	288	9	US-09-925-299-840	Sequence 840, App
19	168	9.4	288	10	US-09-925-299-840	Sequence 840, App
20	168	9.4	288	14	US-10-106-698-4522	Sequence 4522, Ap
21	168	9.4	288	14	US-10-106-698-6263	Sequence 6263, Ap
22	168	9.4	443	14	US-10-396-943-1	Sequence 1, Appli
23	167	9.3	254	14	US-10-216-408-21	Sequence 21, Appl
24	167	9.3	255	9	US-09-864-711-15	Sequence 15, Appl
25	167	9.3	262	9	US-09-981-353-63	Sequence 63, Appl
26	165	9.2	273	14	US-10-314-669-233	Sequence 233, App
27	164	9.1	261	15	US-10-295-027-460	Sequence 460, App
28	163.5	9.1	288	15	US-10-310-154-607	Sequence 607, App
29	146.5	8.2	378	16	US-10-389-566-364	Sequence 364, App
30	143.5	8.0	178	11	US-09-864-408A-3000	Sequence 3000, Ap
31	126	7.0	263	14	US-10-396-943-12	Sequence 12, Appl
32	121.5	6.8	590	15	US-10-369-493-1707	Sequence 1707, Ap
33	112	6.2	453	15	US-10-369-493-14065	Sequence 14065, A
34	111.5	6.2	124	10	US-09-989-442-96	Sequence 96, Appl
35	111.5	6.2	124	10	US-09-989-442-142	Sequence 142, App
36	108.5	6.0	442	14	US-10-156-761-9153	Sequence 9153, Ap
37	108	6.0	178	9	US-09-925-301-914	Sequence 914, App
38	107	6.0	543	14	US-10-156-761-14563	Sequence 14563, A
39	106.5	5.9	450	9	US-09-795-693-34	Sequence 34, Appl
40	106.5	5.9	450	14	US-10-156-239-34	Sequence 34, Appl
41	106.5	5.9	450	14	US-10-199-485-34	Sequence 3, Appli
42	105.5	5.9	633	9	US-09-834-998A-3	Sequence 3651, Ap
43	105	5.9	252	9	US-09-738-626-3651	Sequence 5741, Ap
44	105	5.9	476	9	US-09-738-626-5741	Sequence 34, Appl
45	103	5.7	454	9	US-09-895-913A-34	

ALIGNMENTS

RESULT 1  
US-09-849-980B-1  
; Sequence 1, Application US/09849980B  
; Patent No. US20020123611A1  
; GENERAL INFORMATION:  
; APPLICANT: SANTEN PHARMACEUTICAL CO., LTD.  
; TITLE OF INVENTION: No. US20020123611A1 Polypeptide Having Water Channel  
; TITLE OF INVENTION: Activity and DNA sequence  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SANTEN PHARMACEUTICAL CO., LTD.  
; STREET: 9 19 Shimoshinjo 3-chome Higashiyodogawa-Ku  
; CITY: Osaka  
; STATE: Osaka  
; COUNTRY: JAPAN  
; ZIP: 533-0021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB, storage  
; COMPUTER: IBM PS/2 or compatibles  
; OPERATING SYSTEM: WINDOWS 95/97  
; SOFTWARE: Microsoft Word 97  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/849,980B  
; FILING DATE: 19-OCT-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP98/01371  
; FILING DATE: 27-MAR-1998  
; APPLICATION NUMBER: JP 09-094845  
; FILING DATE: 28-MAR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Burton A. Amernick  
; REGISTRATION NUMBER: 24852  
; REFERENCE/DOCKET NUMBER: 1581/00156  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)331-7111  
; TELEFAX: (202)293-6229  
; INFORMATION FOR SEQ ID NO: 1:

*[Handwritten signature]*

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 342 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-849-980B-1

Query Match 100.0%; Score 1794; DB 9; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.8e-174;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVQASGHRSTRSGKMSWSVIAKIQEILQRKMVREFLAEFMSTYVMVFGLSVAHMLV 60
   |||
Db 1 MVQASGHRSTRSGKMSWSVIAKIQEILQRKMVREFLAEFMSTYVMVFGLSVAHMLV 60

Qy 61 NKKGYSYLGVLGFGFGVTMGVHVAGRISGAHMNAAVTFANCALGRVPWRKFPVYVLGQF 120
   |||
Db 61 NKKGYSYLGVLGFGFGVTMGVHVAGRISGAHMNAAVTFANCALGRVPWRKFPVYVLGQF 120

Qy 121 LGSFLAAATYISLFYTAILHFSGGQLMVTGPVAFAGIFATYLPDHMTLWRGFLNEAWLTG 180
   |||
Db 121 LGSFLAAATYISLFYTAILHFSGGQLMVTGPVAFAGIFATYLPDHMTLWRGFLNEAWLTG 180

Qy 181 MLQLCLFATTDQENNPALPGTEALVIGILVVIIGVSLGMNTGYAINPSRDLPPRIFTFIA 240
   |||
Db 181 MLQLCLFATTDQENNPALPGTEALVIGILVVIIGVSLGMNTGYAINPSRDLPPRIFTFIA 240

Qy 241 GWGKQVFSNGENWWVPVAPLLGAYLGGIYLVFVGSTIPREPLKLEDSVAYEDHGITV 300
   |||
Db 241 GWGKQVFSNGENWWVPVAPLLGAYLGGIYLVFVGSTIPREPLKLEDSVAYEDHGITV 300

Qy 301 LPRKGSHEPTISPLTPVSVSPANRSSVHPAPPLHESMALEHF 342
   |||
Db 301 LPRKGSHEPTISPLTPVSVSPANRSSVHPAPPLHESMALEHF 342

RESULT 2
US-10-093-463-174
; Sequence 174, Application US/10093463
; Publication No. US20030208039A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shenoy, Suresh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Gusev, Vladimir
; APPLICANT: Pochart, Pascal
; APPLICANT: Zhong, Mei
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glennnda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gerlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangolli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Pena, Carol
; APPLICANT: Burgess, Catherine
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly
; APPLICANT: Gorman, Linda
; APPLICANT: Spaderna, Steven
; APPLICANT: Voss, Edward
; APPLICANT: Malyankar, Uriel
; APPLICANT: Anderson, David
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; TITLE OF INVENTION: NO. US20030208039A1el Antibodies that Bind to Antigenic Polypepti
; TITLE OF INVENTION: Encoding The Antigens, and Methods of Use.
```

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; FILE REFERENCE: 21402-290A (Cura 590AT)
; CURRENT APPLICATION NUMBER: US/10/093,463
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/283,675
; PRIOR FILING DATE: 2001-04-14
; PRIOR APPLICATION NUMBER: 60/338,092
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/274,101
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/325,681
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/304,354
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/279,995
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/294,899
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/287,424
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/299,027
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/309,198
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/281,194
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/274,849
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/330,380
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/275,235
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/288,342
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 60/275,578
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 370
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 174
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-093-463-174

Query Match 90.9%; Score 1631; DB 15; Length 346;
Best Local Similarity 91.3%; Pred. No. 7.8e-158;
Matches 316; Conservative 7; Mismatches 19; Indels 4; Gaps 1;

Qy 1 MVQASGHRSTRSGKMSWSVIAKIQEIL----QRKMVREFLAEFMSTYVMVFGLSVA 56
   |||
Db 1 MVQASGHRSTRSGKMSWSVIAKIQEIWCEEDERKMVREFLAEFMSTYVMVFGLSVA 60

Qy 57 HMLNKKYGSYLGVLGFGFGVTMGVHVAGRISGAHMNAAVTFANCALGRVPWRKFPVYV 116
   |||
Db 61 HMLNKKYGSYLGVLGFGFGVTMGVHVAGRISGAHMNAAVTFNCALGRVPWRKFPVHV 120

Qy 117 LGQFLGSFLAAATYISLFYTAILHFSGGQLMVTGPVATAGIFATYLPDHMTLWRGFLNEA 176
   |||
Db 121 LGQFLGSFLAAATYISLFYSAILHFSGGELMVTGPFATAGIFATYLPDHMTLWRGFLNEE 180

Qy 177 WLTGMLQLCLFATTDQENNPALPGTEALVIGILVVIIGVSLGMNTGYAINPSRDLPPRIF 236
   |||
Db 181 WLTRMLQLCLFTITDQENNPALPGTHALVISILVVIIRVSHGINTGYAINPSRDPSPSIF 240

Qy 237 TFIAGWGKQVFSNGENWWVPVAPLLGAYLGGIYLVFIGSTIPREPLKLEDSVAYEDH 296
   |||
Db 241 TFIAGWGKQVFSNGENWWVPVAPLLGAYLGGIYLVFIGSTIPREPLKLEDSVAYEDH 300

Qy 297 GITVLPKMGSHPTISPLTPVSVSPANRSSVHPAPPLHESMALEHF 342
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; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 14729
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-14729

Query Match      24.1%; Score 432.5; DB 14; Length 281;
Best Local Similarity 36.6%; Pred. No. 1.3e-35;
Matches 98; Conservative 45; Mismatches 102; Indels 23; Gaps 6;

QY 33 MVRFLAEFMSTYVMVFGLSVVAHMLNKK-----YGSYLGVLNLFSGFGVTMGVHVA 85
Db 10 LIGLSAEFAGTMIILFGAGVVAQVAGGALTTPPGGLGNHDSIAWAWGIGVTMGVYVA 69

QY 86 GRISGAHMAAATFANCALGRVPMRKFPPVYVLGQFLGSFLAAATYSLFYTAILHFSGGQ 145
Db 70 ARLSGAHLNPAVTTLAAAFKGFPMKSVAPYAVAQTLGAFVAALLVRWNYTEALAKADPGH 129

QY 146 LMTGCVATAGIFATY-----LPDHMTLWRGFLNEAWLTGMLQLCLFATTDQENNPAL 198
Db 130 TL-----KTQGVFSTLPANGPNLPVHE--WGAFRDQVIGTAILLLILAITDLLNTPPG 182

QY 199 PGTEALVIGILVIGVSLGMNTGYAINPSRDLPPRIFTFIAGWKQVFSN-GENWWWVP 257
Db 183 ANLAPFIIGLVVAIGMAWGTNAGYAINPARDFGPRLASFITGYSAWRDQYGNFYFWVP 242

QY 258 VVAPLLGAYLGIIYLVFIGSTIP-REP 284
Db 243 IIGPLIGLLGGVVYKFFVGVGRFLPTAEP 270
```

```

RESULT 6
US-10-156-761-14492
; Sequence 14492, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 14492
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-14492

Query Match      17.9%; Score 321.5; DB 14; Length 249;
Best Local Similarity 34.1%; Pred. No. 2.3e-24;
Matches 87; Conservative 43; Mismatches 94; Indels 31; Gaps 10;

QY 37 FLAEFMSTYVMVFGLSVVAHMLV---NKKYGSYLGVLNLFSGFGVTMGVHVAGRISGAHM 93
Db 7 FVGEIIGTAILILFGAGVCAAVTLRYSKARASGWVIAFGWFGVGLAGAYTAAPLSGGHL 66
```

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QY 94 NAAVTFANCALGRVPMRKFPPVYVLGQFLGSFLAAATYSLF---YTAILHFSG-QQLMVT 149
Db 67 NPAVTI-GIAIDTGTWGVKVIYLLGQLVGAVLGAVLAYLVLAQFQANVRKEGTETGAD 125

QY 150 GPVATAGIFATYLPDHMTLWRGFLNE--AWLTGMLQLCLFATTDQENNPALPGTEALVIG 207
Db 126 EPVPTLGIFST-IPEIRNPVANLITEIIATIALVLPILAFGLT---KGLGESGITVLIVS 181

QY 208 ILVVIIGVSLGMNTGYAINPSRDLPPRI-FTPI-----AGWKQVFSNGENWWWVPV 259
Db 182 LLVVGIGLSLGGPTGYAINPARDLGPRIVHTFLPIPNKGTSDWG-----YAWIPVV 232

QY 260 APLLGAYLGIIYLV 274
Db 233 GPLIGGALAGLIYHV 247

RESULT 7
US-10-156-761-14193
; Sequence 14193, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 14193
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-14193

Query Match      17.2%; Score 308.5; DB 14; Length 264;
Best Local Similarity 32.6%; Pred. No. 5.4e-23;
Matches 85; Conservative 43; Mismatches 104; Indels 29; Gaps 8;

QY 37 FLAEFMSTYVMVFGLSVVAHMLV---NKKYGSYLGVLNLFSGFGVTMGVHVAGRISGAHM 93
Db 7 FIGETIGTAVLILGGGVCAAVTLKASKARNAGWLAITFGWGAFLVTAVYISAPLSGAHL 66

QY 94 NAAVTFANCALGRVPMRKFPPVYVLGQFLGSFLAAATYSLFYTAI-LHFSGGQLMVTGPV 152
Db 67 NPAVTLA-LAIKNDWSNVPTYWAGQLLGAMIGAALVWVAYYQGFHAHLTDHEI-VGGPG 124

QY 153 ATA-----GIFATYLPDHMTLWRGFLNEAWLTGMLQLCLFATTDQENN 195
Db 125 AOATKTKAVERAQTGAGPVLGVFSTG-PEVRNVVNQLATEIIGTVVLVLAILTQGLNDNG 183

QY 196 PALPGTEALVIGILVVIIGVSLGMNTGYAINPSRDLPPRIFTFIAGWKQVFSNGENW-- 253
Db 184 NGLGTIGALITSLVWVSIGLSGGPTGYAINPARDLGPRIVHALLPLPNK---GGSDWSY 240

QY 254 WVPVVPAPLLGAYLGIIYLV 274
Db 241 AWIPVVGPLIGAAIAAGIYNV 261
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RESULT 8
US-09-769-787-9
; Sequence 9, Application US/09769787
; Publication No. US20030091577A1
```

GENERAL INFORMATION:  
APPLICANT: Microbial Technics Limited  
APPLICANT: Gilbert, Christophe FG  
APPLICANT: Hansbro, Philip M  
TITLE OF INVENTION: Proteins  
FILE REFERENCE: PWC/P21129WO  
CURRENT APPLICATION NUMBER: US/09/769,787  
CURRENT FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: GB 9816337.1  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: US 60/125164  
PRIOR FILING DATE: 1999-03-19  
NUMBER OF SEQ ID NOS: 388  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 9  
LENGTH: 234  
TYPE: PRT  
ORGANISM: Streptococcus pneumoniae  
US-09-769-787-9

Query Match 17.1%; Score 307.5; DB 10; Length 234;  
Best Local Similarity 32.5%; Pred. No. 5.7e-23;  
Matches 83; Conservative 49; Mismatches 90; Indels 33; Gaps 10;

Qy 33 MVREFLAEFMSTYVMVFGLSVAHMLNKKYGYLG---VNLGFGFGVTMGVHVAGRIS 89  
Db 1 MNVELFGEFLGTLILLLGNWVAGVLPKTKSNSSGWIIVTMGWIAGVAVFVSGKLS 60

Qy 90 GAHMAAAVTFANCALGRVPRKFPVYVLGQFLGSFLAAATISLF---YTAILHFSGGQL 146  
Db 61 PAYLNPVAVTIGVALKGLPWASVLPYILAQFAGAMLGQILVWLQFKPHYEA--EENAGNI 118

Qy 147 MV---TGPVATAGIFATYLPDHMTLWRGFLNEAWLTGMLQCLFATTDQENNPALPGTEA 203  
Db 119 LATFSTGPA-----IKDVS---NLISEILGTFLVLTIFALGLYDFQAGI-GTFA 165

Qy 204 LVIGILVVIIGVSLGNTGYAINPSRDLPPRIFTFIAGWGKQVFSNGENWW---WVPVVA 260  
Db 166 --VGTLLVIGLSLGGTTGYALNPARDLGRIMHSIL----PIPNKGDGDSYAWIPVVG 219

Qy 261 PLLGAYLGGIYLVF 275  
Db 220 PVIGAALAVLVESLF 234

RESULT 9  
US-10-029-386-27867  
Sequence 27867, Application US/10029386  
Publication No. US20030194704A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO  
FILE REFERENCE: AEOMICA-X-2  
CURRENT APPLICATION NUMBER: US/10/029,386  
CURRENT FILING DATE: 2001-12-20  
NUMBER OF SEQ ID NOS: 34288  
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 27867  
LENGTH: 58  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AL137070.3  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.81  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.94  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.55  
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.65  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.72  
OTHER INFORMATION: SWISSPROT HIT: O14520, EVALUATION 2.00e-24

US-10-029-386-27867

Query Match 15.0%; Score 269; DB 14; Length 58;  
Best Local Similarity 93.1%; Pred. No. 7e-20;  
Matches 54; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 269 GIIYLVFIGSTIPREPLKLEDSVAYEDHGITVLPKMGSHPTISPLTPVSVSPANRSS 326  
Db 1 GIIYLVFIGSTIPREPLKLEDSVAYEDHGITVLPKMGSHPTISPLTPVSVSPANRSS 58

RESULT 10  
US-10-295-027-254  
Sequence 254, Application US/10295027  
Publication No. US20030232350A1  
GENERAL INFORMATION:  
APPLICANT: Afar, Daniel  
APPLICANT: Aziz, Natasha  
APPLICANT: Ginsberg, Wendy M.  
APPLICANT: Gish, Kurt C.  
APPLICANT: Glynn, Richard  
APPLICANT: Hevezi, Peter A.  
APPLICANT: Mack, David H.  
APPLICANT: Murray, Richard  
APPLICANT: Watson, Susan R.  
APPLICANT: Eos Biotechnology, Inc.  
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and  
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer  
FILE REFERENCE: 018501-012500US  
CURRENT APPLICATION NUMBER: US/10/295,027  
CURRENT FILING DATE: 2002-11-13  
PRIOR APPLICATION NUMBER: US 09/663,733  
PRIOR FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: US 60/350,666  
PRIOR FILING DATE: 2001-11-13  
PRIOR APPLICATION NUMBER: US 60/335,394  
PRIOR FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: US 60/332,464  
PRIOR FILING DATE: 2001-11-21  
PRIOR APPLICATION NUMBER: US 60/334,393  
PRIOR FILING DATE: 2001-11-29  
PRIOR APPLICATION NUMBER: US 60/340,376  
PRIOR FILING DATE: 2001-12-14  
PRIOR APPLICATION NUMBER: US 60/347,211  
PRIOR FILING DATE: 2002-01-08  
PRIOR APPLICATION NUMBER: US 60/347,349  
PRIOR FILING DATE: 2002-01-10  
PRIOR APPLICATION NUMBER: US 60/355,250  
PRIOR FILING DATE: 2002-02-08  
PRIOR APPLICATION NUMBER: US 60/356,714  
PRIOR FILING DATE: 2002-02-13  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 1386  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 254  
LENGTH: 323  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-295-027-254

Query Match 13.2%; Score 236.5; DB 15; Length 323;  
Best Local Similarity 28.6%; Pred. No. 1.6e-15;  
Matches 71; Conservative 36; Mismatches 88; Indels 53; Gaps 9;

Qy 39 AEFMSTYVMVFGLSVAH-----MVLNKKYGYLVGNLGFVGVTMGVHVAGR 87  
Db 40 AEFLAMLI FVLLSLGSTINWGTEKPLPVDML-----ISLCFGLSIATMVQCFGH 90

Qy 88 ISGAHMAAAVTFANCALGRVPRKFPVYVLGQFLGSFLAAATISLFTAILHFSGGQLM 147  
Db 91 ISGGHINPAVTAMVCTRKISIAKSVFYIAAQCLGAIIGAGILY-----L 135

Qy 148 VTGPVATAGIFATYLPDHMTLWRGFLNEAWLTGMLQCLFATTDQENNPALPGTEALVIG 207

Db 136 VTPSVVGLGVTVMHGNLTAGHLLVELIITFQLVFTIFASCDSKRTD-VTGSIALAIG 194  
Qy 208 ILVVIGVSLGMN-TGYAINPSRDLPPRIFFTFIAGWGKQVFSNGENWW--WVPVVAPLL 264  
Db 195 FSVA-IGHLFAINTGASMPARSGPAV-----IMGNWENHWIYW---VGPIIG 240  
Qy 265 AYLGGLIY 272  
Db 241 AVLAGGLY 248

RESULT 11  
US-10-097-340-12  
; Sequence 12, Application US/10097340  
; Publication No. US20030087250A1  
; GENERAL INFORMATION:  
; APPLICANT: John MONAHAN  
; APPLICANT: Manjula GANNAVAPURU  
; APPLICANT: Sebastian HOERSCH  
; APPLICANT: Shubhangi KAMATKAR  
; APPLICANT: Steve G. KOVATS  
; APPLICANT: Rachel E. MEYERS  
; APPLICANT: Michael MORRISEY  
; APPLICANT: Peter OLANDT  
; APPLICANT: Ami SEN  
; APPLICANT: Peter VEIBY  
; APPLICANT: Gordon B. MILLS  
; APPLICANT: Robert C. BAST, Jr.  
; APPLICANT: Karen LU  
; APPLICANT: Rosemarie SCHMANDT  
; APPLICANT: Xumei ZHAO  
; APPLICANT: Karen GLATT  
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,  
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer  
; FILE REFERENCE: MRI-030  
; CURRENT APPLICATION NUMBER: US/10/097,340  
; CURRENT FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: 60/276,025  
; PRIOR FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: 60/325,149  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 60/276,026  
; PRIOR FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: 60/324,967  
; PRIOR FILING DATE: 2001/09/26  
; PRIOR APPLICATION NUMBER: 60/311,732  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/325,102  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 60/323,580  
; PRIOR FILING DATE: 2001-09-19  
; NUMBER OF SEQ ID NOS: 363  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 265  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-097-340-12

Query Match 12.6%; Score 226.5; DB 14; Length 265;  
Best Local Similarity 27.4%; Pred. No. 1.3e-14;  
Matches 80; Conservative 45; Mismatches 110; Indels 57; Gaps 11;  
Qy 26 QEILQRKRVREFLAEFMSTYVMVFGLSVAHMLNKKYGS-----YLGVNLFSGFGVTMG 81  
Db 3 KEVCSVAFKAVFAEFLATLIFVFFGLGSAL-----KWPSALPTILQIALAFGLAIGTL 56  
Qy 82 VHVAGRISGAHMAAATFANCALGRVPWRKFPVYVLGQFLGSFLAAATYISLFYTAILHF 141  
Db 57 AQALGPVSGGHINPAITLALLVGNQISLLRAFFYVAAQLVGAAGAGILYGV----- 108  
Qy 142 SGGQLMVTGPVATAGIFA-TYLPDHMTLWRGFLNEAWLTGMLQLCLFATTDQENNPALPG 200

Db 109 -----APLNARGNLAVNALNNNTTQGOAMVVELILTFQLALCIFASTDSRRTSPV-G 159  
Qy 201 TEALVIGILVVIIGVSLGMN-TGYAINPSRDLPPRIFFTFIAGWGKQVFSNGENWWVPV 259  
Db 160 SPALSIG-LSVTLGHVGIYFTGCSMNPARGPAV-----VMNRFSPAHWVFW 208  
Qy 260 APLLGAYLGGII--YLVFIGSTIPREPLKLEDSVAYEDHGITVLPKMGSH 309  
Db 209 GPIVGAVLAAILYFYLLFPNS-----LSLSERVAI-----IKGTYP 245  
RESULT 12  
US-10-171-311-16  
; Sequence 16, Application US/10171311  
; Publication No. US20030087270A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlegel, Robert  
; APPLICANT: Chen, Yan  
; APPLICANT: Zhao, Xumei  
; APPLICANT: Monahan, John  
; APPLICANT: Kamatkar, Shubhangi  
; APPLICANT: Glatt, Karen  
; APPLICANT: Gannavarapu, Manjula  
; APPLICANT: Hoersh, Sebastian  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR  
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY  
; TITLE OF INVENTION: OF CERVICAL CANCER  
; FILE REFERENCE: MRI-035  
; CURRENT APPLICATION NUMBER: US/10/171,311  
; CURRENT FILING DATE: 2002-06-12  
; PRIOR APPLICATION NUMBER: US 60/298,159  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: US 60/298,155  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: US 60/335,936  
; PRIOR FILING DATE: 2001-11-14  
; NUMBER OF SEQ ID NOS: 238  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 265  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-171-311-16

Query Match 12.6%; Score 226.5; DB 14; Length 265;  
Best Local Similarity 27.4%; Pred. No. 1.3e-14;  
Matches 80; Conservative 45; Mismatches 110; Indels 57; Gaps 11;  
Qy 26 QEILQRKRVREFLAEFMSTYVMVFGLSVAHMLNKKYGS-----YLGVNLFSGFGVTMG 81  
Db 3 KEVCSVAFKAVFAEFLATLIFVFFGLGSAL-----KWPSALPTILQIALAFGLAIGTL 56  
Qy 82 VHVAGRISGAHMAAATFANCALGRVPWRKFPVYVLGQFLGSFLAAATYISLFYTAILHF 141  
Db 57 AQALGPVSGGHINPAITLALLVGNQISLLRAFFYVAAQLVGAAGAGILYGV----- 108  
Qy 142 SGGQLMVTGPVATAGIFA-TYLPDHMTLWRGFLNEAWLTGMLQLCLFATTDQENNPALPG 200  
Db 109 -----APLNARGNLAVNALNNNTTQGOAMVVELILTFQLALCIFASTDSRRTSPV-G 159  
Qy 201 TEALVIGILVVIIGVSLGMN-TGYAINPSRDLPPRIFFTFIAGWGKQVFSNGENWWVPV 259  
Db 160 SPALSIG-LSVTLGHVGIYFTGCSMNPARGPAV-----VMNRFSPAHWVFW 208  
Qy 260 APLLGAYLGGII--YLVFIGSTIPREPLKLEDSVAYEDHGITVLPKMGSH 309  
Db 209 GPIVGAVLAAILYFYLLFPNS-----LSLSERVAI-----IKGTYP 245

RESULT 13  
US-09-867-550-282  
; Sequence 282, Application US/09867550

Patent No. US20020082206A1  
; GENERAL INFORMATION:  
; APPLICANT: Leach, Martin D.  
; APPLICANT: Mehraban, Fuad,  
; APPLICANT: Conley, Pamela  
; APPLICANT: Law, Debbie  
; APPLICANT: Topper, James  
; TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells and  
; FILE OF INVENTION: Thereby  
; FILE REFERENCE: 21402-013 (Cura-313)  
; CURRENT APPLICATION NUMBER: US/09/867,550  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: USSN 60/208,427  
; PRIOR FILING DATE: 2000-05-30  
; NUMBER OF SEQ ID NOS: 2125  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 282  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)  
; OTHER INFORMATION: wherein Xaa may be any one of Leu or Ser or Trp or Pro or Gln or  
; OTHER INFORMATION: Met or Thr or Lys or Val or Ala or Glu or Gly  
; NAME/KEY: VARIANT  
; LOCATION: (23)  
; OTHER INFORMATION: wherein Xaa may be any one of Glu or Gln or Lys  
US-09-867-550-282  
Query Match 11.1%; Score 200; DB 9; Length 107;  
Best Local Similarity 46.2%; Pred. No. 1.8e-12;  
Matches 37; Conservative 14; Mismatches 29; Indels 0; Gaps 0;  
Qy 203 ALVIGILVVIIGVSLGNTGYAINPSRDLPPRIFFIAGWGKQVFSNGENWVVPVAPL 262  
Db 5 ALIIGLLVAAGACAGSSXAWAINPARDLRPGVRFFAGWGESALPGKQNVFVPIVAPL 64  
Qy 263 LGAYLGGIIVLVFIGSTIPR 282  
Db 65 IGGPIGGAIVSPAIRPFLPK 84  
RESULT 14  
US-10-409-701-15  
; Sequence 15, Application US/10409701  
; Publication No. US20030221224A1  
; GENERAL INFORMATION:  
; APPLICANT: Zinselmeier, Chris  
; APPLICANT: Helentjaris, Timothy G.  
; TITLE OF INVENTION: Enhanced Silk Exsertion Under Stress  
; FILE REFERENCE: 1421  
; CURRENT APPLICATION NUMBER: US/10/409,701  
; CURRENT FILING DATE: 2003-04-08  
; PRIOR APPLICATION NUMBER: US 60/370,796  
; PRIOR FILING DATE: 2002-04-08  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15  
; LENGTH: 249  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Xaa = any amino acid  
US-10-409-701-15  
Query Match 10.3%; Score 184; DB 15; Length 249;  
Best Local Similarity 26.6%; Pred. No. 2.5e-10;  
Matches 69; Conservative 41; Mismatches 99; Indels 50; Gaps 11;  
Qy 34 VREFLAEFMSTYVMVFGLSVAHMLNKKYG-----SYLGNLGFQFGVTMGV 82  
Db 18 IKAYVAEFIATLLFVFAVGSAI-----AYGQLTNGGALDPAGLVAIAIAHALALFVG 71

Qy 83 HVAGRISGAHMAAATFANCALGRVPRKFPVYVLGQFLGSFLAAATYSLFYTAILHPS 142  
Db 72 SVAANISGGHLNPAVTGLAVGGHITILTGVFYWVAQLLG-----ATVACLLLGFTVTH-- 124  
Qy 143 GGQLMVTGPVATAGIFATYLPDHTLWRGFLNEAWLTGMLQCLFATTDQENNPALPGTE 202  
Db 125 -GKAIPH--AVAGI-----SELEGVVFEVVITFALVYTVYATAADPKKGSGLGTTA 172  
Qy 203 ALVIGILVVIIGVSLGNTGYAINPSRDLPPRIFFIAGWGKQVFSNGENW--WVVPVAP 261  
Db 173 PIAIGFIVGANILAAAGPFGSGSMNPARSFGPAV---AAG-----DFAGNWWVYW---VGP 220  
Qy 262 LLGAYLGGIIV-LVFIGST 279  
Db 221 LVGGGLAGLVYGDVFIGGS 239  
RESULT 15  
US-10-310-154-606  
; Sequence 606, Application US/10310154  
; Publication No. US20030233670A1  
; GENERAL INFORMATION:  
; APPLICANT: Edgerton, Michael D  
; APPLICANT: Chomet, Paul S.  
; APPLICANT: Adams, Thomas H  
; APPLICANT: Ruff, Thomas G.  
; APPLICANT: Agarwal, Ameeta K.  
; APPLICANT: Ahrens, Jeffrey E.  
; APPLICANT: Ball, James A.  
; APPLICANT: Banu, G.  
; APPLICANT: Bell, Erin  
; APPLICANT: Boddupalli, Raghava  
; APPLICANT: Deikman, Jill  
; APPLICANT: Deng, Molian  
; APPLICANT: Dong, Jinzhao  
; APPLICANT: Duff, Stephen M.  
; APPLICANT: Galligan, Meghan M.  
; APPLICANT: Hinchey, Brenda S.  
; APPLICANT: Huang, Shihshieh  
; APPLICANT: Johnson, G. Richard  
; APPLICANT: Jung, Vincent  
; APPLICANT: Kretzmer, Keith A  
; APPLICANT: Laccetti, Lucille B.  
; APPLICANT: Lai, Chao-Qiang  
; APPLICANT: Lee, Gary  
; APPLICANT: Lin, Jie-Yi  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Lu, Bin  
; APPLICANT: Luethy, Michael M.  
; APPLICANT: Lund, Adrian  
; APPLICANT: Madson, Linda L.  
; APPLICANT: Malloy, Kathleen A.  
; APPLICANT: McKiel, Christine L.  
; APPLICANT: Miller, Philip W.  
; APPLICANT: Padmavathi, Manchikanti  
; APPLICANT: Parnell, Laurence D.  
; APPLICANT: Start, William G.  
; APPLICANT: Tennesen, Dan  
; APPLICANT: Vidya, K.R.  
; APPLICANT: Wang, Haiyun  
; APPLICANT: Xin, Zhanguo  
; APPLICANT: Xu, Nanfei  
; APPLICANT: Yang, Chunzhi  
; APPLICANT: Zeng, Xiaoping  
; APPLICANT: Zhang, Qiang  
; APPLICANT: Zhao, Yajuan  
; APPLICANT: Zhou, Li  
; TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants  
; FILE REFERENCE: 38-15(52796)B  
; CURRENT APPLICATION NUMBER: US/10/310,154  
; CURRENT FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: 60/337,358

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; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 736
; SEQ ID NO 606
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Zea mays
US-10-310-154-606

Query Match      10.3%; Score 184; DB 15; Length 249;
Best Local Similarity 26.6%; Pred. No. 2.5e-10;
Matches 69; Conservative 41; Mismatches 99; Indels 50; Gaps 11;

QY 34 VREFLAEFMSTYVMVFGLGSAHMLNKKYG-----SYLGVNLGFGFGVTMGV 82
Db 18 IKAYVAEFIATLLFPAGVGSIAI-----AYQLTNGGALDPAGLVAIAIAHALALFVG 71

QY 83 HVAGRISGAHMAAATFANCALGRVPWRKFPVYVLGQFLGSFLAAATYISLFYTAILHFS 142
Db 72 SVAANISGGHLNPAVTFGLAVGGHITILTGVFYVVAQLLG-----ATVACLLLGFTVTH-- 124

QY 143 GGQLMVTGPVATAGIFATYLPDHMTLWRGFLNEAWLTGMLQLCLFATTDQENNPALPGTE 202
Db 125 -GKAIPTH--AVAGI-----SELEGVFEVVITFALVYTVYATAADPKKGS LGTIA 172

QY 203 ALVIGILWIIIGVSLGMNTGYAINPSRDLPPRIFTFIAGWKQVFSNGENW-WWVPVVP 261
Db 173 PIAIGPIVGANILAAAGPFSGGSMNPARSFGPAV---AAG-----DPAGNWWVYW---VGP 220

QY 262 LLGAYLGGIYY-LVFIGST 279
Db 221 LVGGGLAGLVYGDVFIGGS 239
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Search completed: February 19, 2004, 21:31:54  
Job time : 592 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 19, 2004, 19:57:38 ; Search time 46 Seconds  
(without alignments)  
383.828 Million cell updates/sec

Title: US-09-849-980B-1  
Perfect score: 1794  
Sequence: 1 MVQASGHRSTRGSKMVSWS.....NRSSVHPAPPLHESMALEHF 342

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1794	100.0	342	3	US-09-381-810A-1
2	427	23.8	309	4	US-09-489-039A-10582
3	416	23.2	303	4	US-09-252-991A-22050
4	413	23.0	328	4	US-09-489-039A-9306
5	394	22.0	319	4	US-09-489-039A-9999
6	386.5	21.5	282	4	US-09-543-681A-8275
7	291.5	16.2	238	4	US-09-107-532A-5419
8	278.5	15.5	271	1	US-08-447-554-4
9	278.5	15.5	271	1	US-08-448-160-4
10	263	14.7	239	4	US-09-134-001C-4165
11	256.5	14.3	249	4	US-09-107-532A-7142
12	250	13.9	242	4	US-09-134-000C-5934
13	246	13.7	209	4	US-09-134-000C-5125
14	232.5	13.0	265	1	US-08-468-763-19
15	232.5	13.0	265	2	US-08-393-996A-19
16	230	12.8	239	4	US-09-372-422A-42
17	226	12.6	295	4	US-09-372-422A-38
18	225	12.5	232	4	US-09-328-352-6245
19	224	12.5	312	4	US-09-252-991A-31853
20	222.5	12.4	263	4	US-09-489-039A-12047
21	219	12.2	294	4	US-09-372-422A-40
22	215	12.0	249	4	US-09-372-448A-6
23	202.5	11.3	262	4	US-09-372-422A-32
24	192	10.7	269	1	US-08-447-554-5
25	192	10.7	269	1	US-08-468-763-17
26	192	10.7	269	1	US-08-448-160-5
27	192	10.7	269	2	US-08-393-996A-17

28	184	10.3	249	4	US-09-372-422A-22	Sequence 22, Appli
29	183.5	10.2	250	3	US-08-654-025-2	Sequence 2, Appli
30	182.5	10.2	250	1	US-08-234-939-2	Sequence 2, Appli
31	182.5	10.2	250	1	US-08-558-865-2	Sequence 2, Appli
32	182.5	10.2	250	3	US-08-654-025-7	Sequence 7, Appli
33	180	10.0	296	4	US-09-372-422A-20	Sequence 20, Appli
34	179	10.0	288	4	US-09-372-448A-2	Sequence 2, Appli
35	179	10.0	289	4	US-09-372-422A-2	Sequence 2, Appli
36	179	10.0	292	4	US-09-372-422A-4	Sequence 4, Appli
37	175	9.8	288	4	US-09-372-422A-12	Sequence 12, Appli
38	173	9.6	288	4	US-09-372-422A-14	Sequence 14, Appli
39	172	9.6	288	4	US-09-372-422A-16	Sequence 16, Appli
40	170	9.5	292	4	US-09-372-422A-10	Sequence 10, Appli
41	169	9.4	288	4	US-09-372-422A-18	Sequence 18, Appli
42	168	9.4	257	4	US-09-372-422A-28	Sequence 28, Appli
43	168	9.4	443	4	US-09-610-906-1	Sequence 1, Appli
44	167	9.3	262	4	US-09-976-594-347	Sequence 347, App
45	167	9.3	284	4	US-09-372-448A-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1  
US-09-381-810A-1  
; Sequence 1, Application US/09381810A  
; Patent No. 6252046  
; GENERAL INFORMATION:  
; APPLICANT: SANTEN PHARMACEUTICAL CO., LTD.  
; TITLE OF INVENTION: No. 6252046el Polypeptide Having Water Channel  
; TITLE OF INVENTION: Activity and DNA sequence  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SANTEN PHARMACEUTICAL CO., LTD.  
; STREET: 9 19 Shimoshinjo 3-chome Higashiyodogawa-Ku  
; CITY: Osaka  
; STATE: Osaka  
; COUNTRY: JAPAN  
; ZIP: 533-0021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB, storage  
; COMPUTER: IBM PS/2 or compatibles  
; OPERATING SYSTEM: WINDOWS 95/97  
; SOFTWARE: Microsoft Word 97  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/381,810A  
; FILING DATE: 19-OCT-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP09 094845  
; FILING DATE: 28-MAR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Burton A. Amernick  
; REGISTRATION NUMBER: 24852  
; REFERENCE/DOCKET NUMBER: 1581/00156  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)331-7111  
; TELEFAX: (202)293-6229  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 342 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-381-810A-1

Query Match 100.0%; Score 1794; DB 3; Length 342;  
Best Local Similarity 100.0%; Pred. No. 9.6e-186;  
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVQASGHRSTRGSKMVSWSVIAKIQEILQKMKVREFLAEFMSTYVMVFGLSVAHML 60  
Db 1 MVQASGHRSTRGSKMVSWSVIAKIQEILQKMKVREFLAEFMSTYVMVFGLSVAHML 60





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; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...238
; SEQUENCE DESCRIPTION: SEQ ID NO: 5419:
US-09-107-532A-5419

Query Match      16.2%; Score 291.5; DB 4; Length 238;
Best Local Similarity 29.6%; Pred. No. 2.8e-23;
Matches 73; Conservative 50; Mismatches 103; Indels 21; Gaps 6;

QY 36 EFLAEFMSTYVMVFGLSVAHMLNK---KYGSYLGNLGFVGTMGVHVAGRISGAH 92
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 7 QIMGEFIGTLILVLLGDGVCAAVNLNKSQAQASGVIIVAFGWGLAVTMVAVYISGFMGPAH 66

QY 93 MNAAVTFANCALGRVPWRKFPVYVVLGQFLGSFLAAATYISLFTYTAILHFSGGQLMVTGPV 152
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 LNPAVSLAMAMTGAISWNLVVPFIITAQVLGAFAGAILVW--LSYLPHNATKDESAILGTF 125

QY 153 ATAGIFATYLPDHMTLWRGFLNEAWLTGMLQLCLPATTQDQNNPALPGTEALVIGILVVI 212
   || : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 126 ATGPAIRNYPANVITELIG-----TFVLVLGLLAF---GQNEFAPGTNVFAVGGILILA 175

QY 213 IGVSIGMNTGYAINPSRDLPPRIFTFIAGWGKQVFSNGENWW---WVPVWAPLLGAYLGG 269
   || : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 176 IGLSLGGPTGYAINPARDEGRLAHAVL---PIANKGTSWDWYSWVPIAGPMIGAIIV 231

QY 270 IIVLVFI 276
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Db 232 GVYSLMV 238
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RESULT 8
US-08-447-554-4
; Sequence 4, Application US/08447554
; Patent No. 5661003
; GENERAL INFORMATION:
; APPLICANT: FUSHIMI, KIYOHIIDE
; APPLICANT: UCHIDA, SHINICHI
; APPLICANT: SASAKI, SEI
; APPLICANT: MARUMO, FUMIAKI
; TITLE OF INVENTION: WATER CHANNEL
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Ave. NW, Ste. 5500
; CITY: Washington, DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,554
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,365
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 5100-0003.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-447-554-4

Query Match      15.5%; Score 278.5; DB 1; Length 271;
Best Local Similarity 31.9%; Pred. No. 8.6e-22;
Matches 92; Conservative 45; Mismatches 110; Indels 41; Gaps 13;

QY 35 REFLAEFMSTYVMVFGLSVAHMLNKKYGYLVGNLGFVGTMGVHVAGRISGAHNM 94
   || : : : : : : : : : : : : : : : : : : : : : : : : : :
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QY 95 AAVTFANCALG-RVPWRKFPVYVVLGQFLGSFLAAATYISLFTYTAILHFSGGQLMVTGPVA 153
   || : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 69 PAVTVA-CLVGCHVSFLRAAFVAAQLLGAVAGAAILHEI-----TPVE 111

QY 154 TAGIFA-TYLPDHMTLWRGFLNEAWLTGMLQLCLPATTQDQNNPALPGTEALVIGILVVI 212
   || : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 112 IRGDLAVNALHNNATAGQAVTVVELFLTMQLVLCIFASTDERRGDNL-GSPALSIGFSVT- 169

QY 213 IGVSIGMNTGYAINPSRDLPPRIFTFIAGWGKQVFSNGENWWVVPVWAPLLGAYLGGII 271
   : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 170 LGHLLGIYFTGCSMNPARS LAPAVVT-----GK--FDD-----HWVFWIGPLVGAIGSLL 218

QY 272 --YLVFIGSTIPREPLK----LEDSVAYEDHGITVLPKMGSHPTISP 313
   || : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 219 YNYLLFPSAKSLQERLAVLKGLEPDTDWEEVERRRRQSVELHSPQSLP 266
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RESULT 9
US-08-448-160-4
; Sequence 4, Application US/08448160
; Patent No. 5785986
; GENERAL INFORMATION:
; APPLICANT: FUSHIMI, KIYOHIIDE
; APPLICANT: UCHIDA, SHINICHI
; APPLICANT: SASAKI, SEI
; APPLICANT: MARUMO, FUMIAKI
; TITLE OF INVENTION: WATER CHANNEL
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Ave. NW, Ste. 5500
; CITY: Washington, DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,160
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,554
; FILING DATE:
; APPLICATION NUMBER: US 08/126,365
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 5100-0003.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-448-160-4
Query Match 15.5%; Score 278.5; DB 1; Length 271;
Best Local Similarity 31.9%; Pred. No. 8.6e-22;
Matches 92; Conservative 45; Mismatches 110; Indels 41; Gaps 13;

Qy 35 REFLEAFMSTYVMVFGLSVAHMLNKKYGSYLVNLFGLFGFVMTGMVHVAGRISGAHMN 94
Db 11 RAVLAEFLLTLFVFFGLGSALQWASSPP--SVLQIAVAFGLGIGILVQALGHVSGAHN 68

Qy 95 AAVTFANCALG-RVPWRKFPVYVVLGQFLGSLAAATYISLFTAILHFSGGQLMVTGPVA 153
Db 69 PAVTVA-CLVGCHVSFLRAAFYVAAQLLGAVAGAAIHAI-----TPVE 111

Qy 154 TAGIFA-TYLPDHMTLWRGFLNEAWLTGMLQLCLFATTDQENNPALPGTEALVIGILVVI 212
Db 112 IRGDLAVNALHNNATAGQAVTVELFLTMQLVCIFASTDERRGDNL-GSPALSIGFSVT- 169

Qy 213 IGVS LGMN-TGYAINPSRDLPPRIFTFIAGWKQVFSNGENWVVPVAPLLGAYLGGII 271
Db 170 LGHLLGIYFTGCSMNPASRLAPAVVT-----GK--FDD----HWVFWIGPLVGAIIIGSL 218

Qy 272 --YLVFIGSTIPREPLK-----LEDSVAYEDHGITVLPKMGSHPTISP 313
Db 219 YNYLLFPSAKSLQERLAVLKGLEPDTDWEEVRRRQSVLHSPQSLP 266

RESULT 10
US-09-134-001C-4165
; Sequence 4165, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4165
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4165
Query Match 14.7%; Score 263; DB 4; Length 239;
Best Local Similarity 35.1%; Pred. No. 3.4e-20;
Matches 74; Conservative 27; Mismatches 86; Indels 24; Gaps 8;

Qy 75 GFGVTMGVHVAGRISGAHMNAAVTFANCALGRVPWRKFPVYVVLGQFLGSLAAATYISLF 134
Db 10 GFGSNNGRLCCWTFSGAHLNPAVTVLAMDGGFSAQVPGYIVCQMLGGIVGVFWLMY 69

Qy 135 YTAILHFSGGQLMVTGPVATAGIFATYLPDHTMLWRGFLNEAWLTGMLQL-CLFATTDQE 193
Db 70 ---LPHWK-----VTEDPAVKLGVPFST-APAIKNYFANFLSEIIGTMALTGILFIGV--- 118

Qy 194 NNPALPGTEALVIGILVVIIGVSLGMNTGYAINPSRDLPPRI---FTFIAGWKQVFSNG 250
Db 119 -NKIADGLNPIIVGSLIIAIGLSLGGTTGYAINPARDLAPRIAHAILPIHGKGK----- 171

Qy 251 ENWWW--VPVAPLLGAYLGGIYLVFIGST 279
Db 172 SNWSYAIVPLGPMAGGMLGAIVYEVFKQT 202

RESULT 11
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```

US-09-107-532A-7142
; Sequence 7142, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneka
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 7142:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 249 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...249
; SEQUENCE DESCRIPTION: SEQ ID NO: 7142:
US-09-107-532A-7142
Query Match 14.3%; Score 256.5; DB 4; Length 249;
Best Local Similarity 28.0%; Pred. No. 1.8e-19;
Matches 79; Conservative 49; Mismatches 89; Indels 65; Gaps 11;

Qy 25 IQEILQRKRVREFLAEFMSTYVMVFGLSVAHMLV--NKKYGS-YLVGNLGFGEVGTMG 81
Db 2 LEVFMYSMLMTRLAEMWIGTALLIIVLGNCAVANVDLKGTKGYGSDWMLIAVGYGFGVMMP 61

Qy 82 VHVAGRISGAHMNAAVTFANCALGRVPWRKFPVYVVLGQFLGSLAAATYISLFTAILHF 141
Db 62 AMIFGGISGNHINPAFTIALASNGLFPWAEVVPYIIAQLIGAAI----- 105

Qy 142 SGGQLMVTGPVATAGIFATYLP-----DHM-----TLWRGFLNEAWLTGML 182
Db 106 --GQLIVV-----ACYKPYDQTDVDNVHVLGTFTSTINSVGSKFNGFVNEFFGSFVL 154

Qy 183 QLCLFATTD---QENNPALPGTEALVIGILVVIIGVSLGMNTGYAINPSRDLPPRIFTF 238
Db 155 FFGALGITKAPFFQDN----LGTALHALGLVWTLVLSLGGPTGPGLNPAFAPRLVHA 210

Qy 239 IAGWKGQVFSNGENWW---WVPVAPLLGAYLGGIY-LVFI 276
Db 211 LL----PLKHKGSSQWGYAWVPVAPICAGVAVFLYKLLFM 248
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RESULT 12  
US-09-134-000C-5934  
; Sequence 5934, Application US/09134000C  
; Patent No. 6617156  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 032796-032  
; CURRENT APPLICATION NUMBER: US/09/134,000C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/055,778  
; PRIOR FILING DATE: 1997-08-15  
; NUMBER OF SEQ ID NOS: 6812  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5934  
; LENGTH: 242  
; TYPE: PRT  
; ORGANISM: Enterococcus faecalis  
US-09-134-000C-5934

Query Match 13.9%; Score 250; DB 4; Length 242;  
Best Local Similarity 30.0%; Pred. No. 8.8e-19;  
Matches 74; Conservative 42; Mismatches 111; Indels 20; Gaps 9;  
QY 33 MYREFLAEFMSTYVMVFGVGLSVAHMVLNK-KY--GSYLVGNLGFVGTMGVHVAGRIS 89  
Db 7 MFHHILSEFMGTALMIVFGVGVHCDVLRXRTKYAGSGHMFATITWAFGISVVLVFG-- 63  
QY 90 GAHMAAATFANCALGRVWPVKFPVYVVGQFLGSFLAAATYISLFYTAILHFSGGQLMVT 149  
Db 64 GVCINPAMALQAAILGMIPWSYFIPYVIAEMLGGICGAVIVIMYAD---HFKLSDSV- 119  
QY 150 GPVATAGIFATYLPDHTLWRGFLNEAWLTGMLQLCLFATTDQENNPALPGTEALVIGIL 209  
Db 120 DPIAIRNIFSTN-PNQRNLPNRYFVETFATFIFLTSILAIA-HSVETQLP----IAVGLL 173  
QY 210 VVIIGVSLGNTGYAINPSRDLPPRIFTFIAGWGKQVFSNGENWVVPVAPLLGAYLGG 269  
Db 174 VWAIGMGLGTTGPFAMNQARDLGPRIAYQLL----PIKNTNNDWQYGLIVPGTAPFLGA 229  
QY 270 IYLVFI 276  
Db 230 IFATLTV 236

RESULT 13  
US-09-134-000C-5125  
; Sequence 5125, Application US/09134000C  
; Patent No. 6617156  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 032796-032  
; CURRENT APPLICATION NUMBER: US/09/134,000C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/055,778  
; PRIOR FILING DATE: 1997-08-15  
; NUMBER OF SEQ ID NOS: 6812  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5125  
; LENGTH: 209  
; TYPE: PRT  
; ORGANISM: Enterococcus faecalis  
US-09-134-000C-5125

Query Match 13.7%; Score 246; DB 4; Length 209;  
Best Local Similarity 31.5%; Pred. No. 1.9e-18;  
Matches 67; Conservative 40; Mismatches 92; Indels 14; Gaps 5;

QY 26 QEILQRKVMREFLAEFMSTYVMVFGVGLSVAHMVLNKK---YGSYLVGNLGFVGTMGV 82  
Db 2 EEKMGTSMTQLFGEFFGTMLVLLGDGVCVAAVNLKSKAFASGWVIALGWAATLAV 61  
QY 83 HVAGRISGAHMAAATFANCALGRVWPVKFPVYVVGQFLGSFLAAATYISLFYTAILHFS 142  
Db 62 YMSGYMSPAHLNPAVTVAITGNFEWGMVLPYIVAQVLGGFVGLVW-LAYLPHWNIT 120  
QY 143 GGQLMVTGPVATAGIFATYLPDHTLWRGFLNEAWLTGMLQLCLFATTDQENNPALPGTE 202  
Db 121 EDKGAILGTATGPAVRNY-PANV-----LTEIIGTFVLVFGLLAFS---QNDLAAAGIN 170  
QY 203 ALVIGILVVIIGVSLGNTGYAINPSRDLPPRI 235  
Db 171 PMLVGILVGLGLSLGGPTGVAINPARDLGPRL 203

RESULT 14  
US-08-468-763-19  
; Sequence 19, Application US/08468763  
; Patent No. 5741671  
; GENERAL INFORMATION:  
; APPLICANT: Agre, Peter C.  
; TITLE OF INVENTION: Isolation, Cloning and Expression of  
; TITLE OF INVENTION: Transmembrane Water Channel Proteins  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Banner & Allegretti  
; STREET: 1001 G Street, N.W.  
; CITY: Washington, D.C.  
; STATE: D.C.  
; COUNTRY: US  
; ZIP: 20001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/468,763  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/393,996  
; FILING DATE: 24-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Posorske, Laurence H.  
; REGISTRATION NUMBER: 34,698  
; REFERENCE/DOCKET NUMBER: 1107.48633  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202 508-9100  
; TELEFAX: 202 508-9299  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 265 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-468-763-19

Query Match 13.0%; Score 232.5; DB 1; Length 265;  
Best Local Similarity 27.6%; Pred. No. 7.9e-17;  
Matches 80; Conservative 44; Mismatches 107; Indels 59; Gaps 11;

QY 26 QEILQRKVMREFLAEFMSTYVMVFGVGLSVAHMVLNKKYGS-----YLVGNLGFVGTMG 81  
Db 3 KEVCSLAFKAVFAEFLATLIFVFFGLGSAL-----KWPSALPTILOISIAFGLAIGTL 56  
QY 82 VHVAGRISGAHMAAATFANCALGRVWPVKFPVYVVGQFLGSFLAAATYISLFYTAILHF 141  
Db 57 AQALGPVSGGHINPAITLALLIGNQISLLRAVFAAQLVGAIAAGILYWL----- 108  
QY 142 SGGQLMVTGPVATAGIFA-TYLPDHTLWRGFLNEAWLTGMLQLCLFATTDQENNPALPG 200



Db 109 -----APLNARGNLAVNALNNNTTPGKAMVVELILITFQLALCIFSSDTSRRTSPV-G 159  
Qy 201 TEALVIGILVVIIGVSLGMN-TGYAINPSRDLPPRIFFTFTAGWKQVFSNGENWWWVPV 259  
Db 160 SPALSIG-LSVTLGHVGIYFTGCSMNPARSFGPAV-----VMNRPSPSHWVFW 208  
Qy 260 APLLGAYLGII--YLVFIGSTIPREPLKLEDSVA-----YEDH 296  
Db 209 GPIVGAMLAAILYFYLLFPSS-----LSLHDRVAVVKGYEPEEDWEDH 252

RESULT 15

US-08-393-996A-19  
; Sequence 19, Application US/08393996A  
; Patent No. 5858702  
; GENERAL INFORMATION:  
; APPLICANT: Agre, Peter C.  
; TITLE OF INVENTION: Isolation, Cloning and Expression of  
; TITLE OF INVENTION: Transmembrane Water Channel Proteins  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Banner & Allegretti  
; STREET: 1001 G Street, N.W.  
; CITY: Washington, D.C.  
; STATE: D.C.  
; COUNTRY: US  
; ZIP: 20001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/393,996A  
; FILING DATE: 24-FEB-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Posorske, Laurence H.  
; REGISTRATION NUMBER: 34,698  
; REFERENCE/DOCKET NUMBER: 1107.48633  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202 508-9100  
; TELEFAX: 202 508-9299  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 265 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-393-996A-19

Query Match 13.0%; Score 232.5; DB 2; Length 265;  
Best Local Similarity 27.6%; Pred. No. 7.9e-17;  
Matches 80; Conservative 44; Mismatches 107; Indels 59; Gaps 11;  
Qy 26 QEILQRMVREFLAEFMSTYVMVFLGSLVSAHMLNKKYGS-----YLGVMLGFGFGVTMG 81  
Db 3 KEVCSLAFKAVFAEFLATLIFVFFGLGSAL-----KWPSALPTILQISIAFGLAIGTL 56  
Qy 82 VHVAGRISGAHMAAATFANCALGRVPWRKFPVYVLGQFLGSFLAAATYISLFYTAILHF 141  
Db 57 AQALGPVSGGHINPAITLALLIGNQISLLRAVFYVAAQLVGAAGILYWL----- 108  
Qy 142 SGGQLMVTGPVATAGIFA-TYLPDHMTLWRGFLNEAWLTGMLQLCLFATTDQENNPALPG 200  
Db 109 -----APLNARGNLAVNALNNNTTPGKAMVVELILITFQLALCIFSSDTSRRTSPV-G 159  
Qy 201 TEALVIGILVVIIGVSLGMN-TGYAINPSRDLPPRIFFTFTAGWKQVFSNGENWWWVPV 259  
Db 160 SPALSIG-LSVTLGHVGIYFTGCSMNPARSFGPAV-----VMNRPSPSHWVFW 208  
Qy 260 APLLGAYLGII--YLVFIGSTIPREPLKLEDSVA-----YEDH 296

Db 209 GPIVGAMLAAILYFYLLFPSS-----LSLHDRVAVVKGYEPEEDWEDH 252  
Search completed: February 19, 2004, 21:15:44  
Job time : 48 secs

